

Tue Dec 3 12:34:35 2002

us-09-848-868-35.max.rge

Page 1

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on:

December 2, 2002, 12:37:43

Search time 2656 seconds
(without alignments)
197.233 Million cell updates/sec

Title: US-09-848-868-35

Sequence:

1 ccggaagcagctctgac 18

Scoring table:

IDENTITY_NUC

Gapop 10.0

Gapext 1.0

Searched:

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database:

GenEmbl:
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_com:*
5: gb_ov:*
6: gb_pat:*
7: gb_pl:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_ov:*
21: em_or:*
22: em_pat:*
23: em_pl:*
24: em_pl:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
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29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_hum:*
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36: em_hlg_hum:*
37: em_hlg_hum:*
38: em_hlg_hum:*
39: em_hlg_hum:*
40: em_hlg_hum:*
41: em_hlg_hum:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	AX298039	AX298039 Sequence
2	17	100.0	36	AX298040	AX298040 Sequence
3	17	94.4	28	I06689	I06689 Sequence 2
4	15	83.3	25	AR003360	AR003360 Sequence
5	14.6	82.2	26	AX053071	AX053071 Sequence
6	13.2	73.3	21	AX464857	AX464857 Sequence
7	12.4	68.9	26	AX464856	AX464856 Sequence
8	12.2	67.8	20	AX348011	AX348011 Sequence
9	12.2	67.8	23	E10818	E10818 FRIC Label1
10	12.2	67.8	26	AR066373	AR066373 Sequence
11	12.2	67.8	33	AX004559	AX004559 Sequence
12	12.2	67.8	33	AX004579	AX004579 Sequence
13	12.2	67.8	33	AX036650	AX036650 Sequence
14	12.2	67.8	50	AX127337	AX127337 Sequence
15	12.2	67.8	22	AR095087	AR095087 Sequence
16	12.2	67.8	23	AR095087	AR095087 Sequence
17	12.2	67.8	24	AR108592	AR108592 Sequence
18	12.2	67.8	26	AX092972	AX092972 Sequence
19	12.2	67.8	26	BD012014	BD012014 Sequence
20	12.2	67.8	26	E55063	E55063 Hydrosoph
21	12.2	67.8	28	BD004494	BD004494 Hydrosoph
22	12.2	67.8	28	BD012788	BD012788 An animal
23	12.2	67.8	28	BD008823	BD008823 An animal
24	12.2	67.8	21	AX332013	AX332013 Sequence
25	12.2	67.8	21	I32023	I32023 Sequence
26	12.2	67.8	21	I32707	I32707 Sequence
27	12.2	67.8	23	AX082157	AX082157 Sequence
28	12.2	67.8	24	AR198876	AR198876 Sequence
29	12.2	67.8	25	AX428028	AX428028 Sequence
30	12.2	67.8	45	AX05137	AX05137 Sequence
31	12.2	67.8	45	AX021010	AX021010 Sequence
32	12.2	67.8	25	E04526	E04526 PCR Primer
33	12.2	67.8	27	AR143851	AR143851 Sequence
34	12.2	67.8	31	AX248747	AX248747 Sequence
35	12.2	67.8	33	AX399412	AX399412 Sequence
36	12.2	67.8	33	AX399412	AX399412 Sequence
37	12.2	67.8	44	AX297519	AX297519 Sequence
38	12.2	67.8	45	AX297519	AX297519 Sequence
39	12.2	67.8	50	AX297519	AX297519 Sequence
40	12.2	67.8	18	A08595	A08595 Sequence
41	12.2	67.8	18	A13808	A13808 Nucleotide syn
42	12.2	67.8	18	BD001730	BD001730 Process F
43	12.2	67.8	21	AR081014	AR081014 Sequence
44	12.2	67.8	21	AR081014	AR081014 Sequence
45	12.2	67.8	25	AX133808	AX133808 Sequence
46	12.2	67.8	26	AX133808	AX133808 Sequence
47	12.2	67.8	26	AX133808	AX133808 Sequence
48	12.2	67.8	28	AX444444	AX444444 Sequence
49	12.2	67.8	28	AR009689	AR009689 Sequence
50	12.2	67.8	33	A25028	A25028 Sequence
51	12.2	67.8	36	AX378843	AX378843 Sequence
52	12.2	67.8	36	AX378843	AX378843 Sequence
53	12.2	67.8	38	AR095087	AR095087 Sequence
54	12.2	67.8	38	AX298227	AX298227 Sequence
55	12.2	67.8	17	AX298227	AX298227 Sequence
56	12.2	67.8	18	AB008824	AB008824 Sequence
57	12.2	67.8	20	AR117660	AR117660 Sequence
58	12.2	67.8	20	AX298335	AX298335 Sequence
59	12.2	67.8	20	AX298335	AX298335 Sequence
60	12.2	67.8	20	E06125	E06125 Primer
61	12.2	67.8	20	E06125	E06125 Primer
62	12.2	67.8	20	E06125	E06125 Primer
63	12.2	67.8	20	E06125	E06125 Primer
64	12.2	67.8	20	E06125	E06125 Primer
65	12.2	67.8	20	E06125	E06125 Primer

C 66	11.2	62.2	21	6	AX119946	AX119946 Sequence	139	10.8	60.0	20	6	AR212409	AR212409 Sequence
C 67	11.2	62.2	24	6	AX111721	AX111721 Sequence	140	10.8	60.0	21	6	AR175671	AR175671 Sequence
C 68	11.2	62.2	24	6	AX111724	AX111724 Sequence	141	10.8	60.0	21	6	AR195247	AR195247 Sequence
C 69	11.2	62.2	24	6	AX148205	AX148205 Sequence	142	10.8	60.0	21	6	AX097226	AX097226 Sequence
C 70	11.2	62.2	24	6	AX148265	AX148265 Sequence	143	10.8	60.0	21	6	AX487105	AX487105 Sequence
C 71	11.2	62.2	24	6	AX119033	AX119033 Sequence	144	10.8	60.0	21	12	ASE251794	ASE251794 Sequence
C 72	11.2	62.2	24	6	AX447009	AX447009 Sequence	145	10.8	60.0	22	6	AR173407	AR173407 Sequence
C 73	11.2	62.2	24	6	BD004779	BD004779 Novel VEG	146	10.8	60.0	22	6	AX097573	AX097573 Sequence
C 74	11.2	62.2	24	6	E38430	E38430 Novel polyP	147	10.8	60.0	23	6	AX426955	AX426955 Sequence
C 75	11.2	62.2	25	6	AR124224	AR124224 Sequence	148	10.8	60.0	24	6	AX088203	AX088203 Sequence
C 76	11.2	62.2	25	6	AR210217	AR210217 Sequence	149	10.8	60.0	25	6	AX278911	AX278911 Sequence
C 77	11.2	62.2	25	6	AR210235	AR210235 Sequence	150	10.8	60.0	25	6	AX426975	AX426975 Sequence
C 78	11.2	62.2	25	6	AX402645	AX402645 Sequence	151	10.8	60.0	26	6	AX037848	AX037848 Sequence
C 79	11.2	62.2	27	6	AX402663	AX402663 Sequence	152	10.8	60.0	26	6	AX466921	AX466921 Sequence
C 80	11.2	62.2	27	6	AR087804	AR087804 Sequence	153	10.8	60.0	26	6	I13498	I13498 Sequence
C 81	11.2	62.2	27	6	AR159648	AR159648 Sequence	154	10.8	60.0	28	6	AR090720	AR090720 Sequence
C 82	11.2	62.2	28	6	AX092072	AX092072 Sequence	155	10.8	60.0	28	6	AR197755	AR197755 Sequence
C 83	11.2	62.2	28	6	AX092090	AX092090 Sequence	156	10.8	60.0	30	6	AR079829	AR079829 Sequence
C 84	11.2	62.2	28	6	AX092173	AX092173 Sequence	157	10.8	60.0	30	6	AX253354	AX253354 Sequence
C 85	11.2	62.2	28	6	AX092896	AX092896 Sequence	158	10.8	60.0	30	6	AX253362	AX253362 Sequence
C 86	11.2	62.2	28	6	I89994	I89994 Sequence	159	10.8	60.0	31	6	AX425508	AX425508 Sequence
C 87	11.2	62.2	29	6	A39955	A39955 Sequence	160	10.8	60.0	32	6	A25771	A25771 sense oligo
C 88	11.2	62.2	29	6	AR054427	AR054427 Sequence	161	10.8	60.0	32	6	AX030669	AX030669 Sequence
C 89	11.2	62.2	29	6	AR167240	AR167240 Sequence	162	10.8	60.0	32	6	I30310	I30310 Sequence
C 90	11.2	62.2	30	6	AX287625	AX287625 Sequence	163	10.8	60.0	34	6	AR179179	AR179179 Sequence
C 91	11.2	62.2	30	6	E32674	E32674 Peptide Inh	164	10.8	60.0	36	6	AR183895	AR183895 Sequence
C 92	11.2	62.2	32	6	AX402994	AX402994 Sequence	165	10.8	60.0	36	6	I08440	I08440 Sequence
C 93	11.2	62.2	32	6	BD011320	BD011320 Human tel	166	10.8	60.0	37	6	AX185857	AX185857 Sequence
C 94	11.2	62.2	32	6	E37069	E37069 Human telom	167	10.8	60.0	40	6	AR169568	AR169568 Sequence
C 95	11.2	62.2	34	6	AX019301	AX019301 Sequence	168	10.8	60.0	40	6	AR183894	AR183894 Sequence
C 96	11.2	62.2	34	6	AX033754	AX033754 Sequence	169	10.8	60.0	40	6	AR018529	AR018529 Sequence
C 97	11.2	62.2	36	6	AR036037	AR036037 Sequence	170	10.8	60.0	40	6	AX018605	AX018605 Sequence
C 98	11.2	62.2	36	6	AR161823	AR161823 Sequence	171	10.8	60.0	40	6	I08439	I08439 Sequence
C 99	11.2	62.2	36	6	AR161834	AR161834 Sequence	172	10.8	60.0	41	6	A38942	A38942 Sequence
C 100	11.2	62.2	36	6	AX378847	AX378847 Sequence	173	10.8	60.0	41	6	AR054338	AR054338 Sequence
C 101	11.2	62.2	36	6	AX378848	AX378848 Sequence	174	10.8	60.0	41	6	AX004844	AX004844 Sequence
C 102	11.2	62.2	36	6	I85715	I85715 Sequence	175	10.8	60.0	42	6	A05118	A05118 Oligonucleo
C 103	11.2	62.2	38	6	AX203574	AX203574 Sequence	176	10.8	60.0	42	6	A33007	A33007 Synthetic P
C 104	11.2	62.2	41	6	AX004845	AX004845 Sequence	177	10.8	60.0	42	6	A33008	A33008 Synthetic P
C 105	11.2	62.2	41	6	BD007098	BD007098 Targeted	178	10.8	60.0	42	6	A33012	A33012 Synthetic P
C 106	11.2	62.2	42	6	AR024300	AR024300 Sequence	179	10.8	60.0	42	6	AX357177	AX357177 Sequence
C 107	11.2	62.2	42	6	AR045153	AR045153 Sequence	180	10.8	60.0	42	6	AX357178	AX357178 Sequence
C 108	11.2	62.2	42	6	AR069547	AR069547 Sequence	181	10.8	60.0	42	6	AX357182	AX357182 Sequence
C 109	11.2	62.2	42	6	BD011377	BD011377 Chimeric	182	10.8	60.0	43	6	AX297642	AX297642 Sequence
C 110	11.2	62.2	42	6	E16947	E16947 PCR primer.	183	10.8	60.0	48	6	A34134	A34134 Synthetic H
C 111	11.2	62.2	42	6	E43847	E43847 Chimeric an	184	10.8	60.0	48	6	A35389	A35389 Synthetic H
C 112	11.2	62.2	44	6	AX297515	AX297515 Sequence	185	10.8	60.0	48	6	A38198	A38198 Sequence
C 113	11.2	62.2	45	6	A03928	A03928 Nucleotide	186	10.8	60.0	48	6	A61805	A61805 Sequence
C 114	11.2	62.2	45	6	A03939	A03939 Nucleotide	187	10.8	60.0	50	6	AR071104	AR071104 Sequence
C 115	11.2	62.2	45	6	A31934	A31934 H.sapiens M	188	10.8	60.0	50	6	AX157852	AX157852 Sequence
C 116	11.2	62.2	48	6	A38199	A38199 Sequence	189	10.8	60.0	50	6	AX158942	AX158942 Sequence
C 117	11.2	62.2	50	6	AX160204	AX160204 Sequence	190	10.8	60.0	50	6	AX159542	AX159542 Sequence
C 118	11.2	62.2	17	6	AR192514	AR192514 Sequence	191	10.6	58.9	18	6	AR154548	AR154548 Sequence
C 119	11.2	62.2	18	6	AR192910	AR192910 Sequence	192	10.6	58.9	18	6	E40623	E40623 RNA virus S
C 120	11.2	62.2	20	6	AR126707	AR126707 Sequence	193	10.6	58.9	19	6	AR154549	AR154549 Sequence
C 121	11.2	62.2	20	6	E15901	E15901 Primer. 7/1	194	10.6	58.9	19	6	AX001207	AX001207 Sequence
C 122	11.2	62.2	21	6	AX095173	AX095173 Sequence	195	10.6	58.9	19	6	AX001209	AX001209 Sequence
C 123	11.2	62.2	27	6	AX179395	AX179395 Sequence	196	10.6	58.9	19	6	AX268649	AX268649 Sequence
C 124	11.2	62.2	31	6	AX259869	AX259869 Sequence	197	10.6	58.9	19	6	AX353624	AX353624 Sequence
C 125	11.2	62.2	31	6	BD002774	BD002774 Gene comp	198	10.6	58.9	19	6	AX353626	AX353626 Sequence
C 126	11.2	62.2	38	6	AR046422	AR046422 Sequence	199	10.6	58.9	19	6	AX393525	AX393525 Sequence
C 127	11.2	62.2	38	6	I53474	I53474 Sequence	200	10.6	58.9	20	6	A07598	A07598 Synthetic a
C 128	11.2	62.2	40	6	I00292	I00292 Sequence	201	10.6	58.9	20	6	AR062641	AR062641 Sequence
C 129	11.2	62.2	42	6	AR032389	AR032389 Sequence	202	10.6	58.9	20	6	AR080260	AR080260 Sequence
C 130	11.2	62.2	42	6	AR209053	AR209053 Sequence	203	10.6	58.9	20	6	AR094445	AR094445 Sequence
C 131	11.2	62.2	42	6	I29129	I29129 Sequence	204	10.6	58.9	20	6	AR104744	AR104744 Sequence
C 132	11.2	62.2	42	6	I90803	I90803 Sequence	205	10.6	58.9	20	6	AR105566	AR105566 Sequence
C 133	10.8	60.0	16	6	AX402876	AX402876 Sequence	206	10.6	58.9	20	6	AR123228	AR123228 Sequence
C 134	10.8	60.0	17	6	AR190541	AR190541 Sequence	207	10.6	58.9	20	6	AR168600	AR168600 Sequence
C 135	10.8	60.0	17	6	AR190542	AR190542 Sequence	208	10.6	58.9	20	6	AX201725	AX201725 Sequence
C 136	10.8	60.0	17	6	AX422374	AX422374 Sequence	209	10.6	58.9	20	6	AX292874	AX292874 Sequence
C 137	10.8	60.0	17	6	AX423069	AX423069 Sequence	210	10.6	58.9	20	6	I20643	I20643 Sequence
C 138	10.8	60.0	20	6	AR174378	AR174378 Sequence	211	10.6	58.9	20	6	I33336	I33336 Sequence

C 212	10.6	58.9	21	6	A48993	A48993 Sequence 5	285	10.6	58.9	47	6	AR058387	AR058387 Sequence
C 213	10.6	58.9	21	6	A87853	A87853 Sequence 1	286	10.6	58.9	47	6	AR088213	AR088213 Sequence
C 214	10.6	58.9	21	6	A89820	A89820 Sequence 1	287	10.6	58.9	47	6	AX194735	AX194735 Sequence
C 215	10.6	58.9	21	6	AR076438	AR076438 Sequence	288	10.6	58.9	48	6	E13196	E13196 Oligonucleo
C 216	10.6	58.9	21	6	AR147757	AR147757 Sequence	289	10.6	58.9	49	6	AR144981	AR144981 Sequence
C 217	10.6	58.9	21	6	AR154542	AR154542 Sequence	290	10.6	58.9	49	6	AX050469	AX050469 Sequence
C 218	10.6	58.9	21	6	AX096828	AX096828 Sequence	291	10.6	58.9	50	6	108628	108628 Sequence 29
C 219	10.6	58.9	21	6	AX476968	AX476968 Sequence	292	10.6	58.9	50	6	AX159200	AX159200 Sequence
C 220	10.6	58.9	21	6	A14621	A14621 Sequence 8	293	10.6	58.9	50	6	AX164949	AX164949 Sequence
C 221	10.6	58.9	22	6	AR102184	AR102184 Sequence	294	10.6	58.9	50	6	AX202538	AX202538 Sequence
C 222	10.6	58.9	22	6	AR204438	AR204438 Sequence	295	10.6	58.9	50	10	MM078813	MM078813 Mus muscul
C 223	10.6	58.9	23	6	A24437	A24437 Oligonucleo	296	10.4	57.8	15	6	AR041381	AR041381 Sequence
C 224	10.6	58.9	23	6	AR096973	AR096973 Sequence	297	10.4	57.8	15	6	AR056170	AR056170 Sequence
C 225	10.6	58.9	24	6	AR044498	AR044498 Sequence	298	10.4	57.8	15	6	AR113928	AR113928 Sequence
C 226	10.6	58.9	24	6	AR048598	AR048598 Sequence	299	10.4	57.8	18	6	A26518	A26518
C 227	10.6	58.9	24	6	AX288211	AX288211 Sequence	300	10.4	57.8	18	6	AR012652	AR012652 Sequence
C 228	10.6	58.9	24	6	AX447031	AX447031 Sequence	301	10.4	57.8	18	6	AR042291	AR042291 Sequence
C 229	10.6	58.9	24	6	ES8780	ES8780 Novel human	302	10.4	57.8	18	6	AR067049	AR067049 Sequence
C 230	10.6	58.9	24	6	A13402	A13402 Sequence 7	303	10.4	57.8	18	6	AR096782	AR096782 Sequence
C 231	10.6	58.9	26	6	A14855	A14855 Nucleotide	304	10.4	57.8	18	6	AX020707	AX020707 Sequence
C 232	10.6	58.9	26	6	AR000039	AR000039 Sequence	305	10.4	57.8	20	6	AR004680	AR004680 Sequence
C 233	10.6	58.9	26	6	AR090896	AR090896 Sequence	306	10.4	57.8	20	6	AR008166	AR008166 Sequence
C 234	10.6	58.9	26	6	AR197931	AR197931 Sequence	307	10.4	57.8	20	6	AR067269	AR067269 Sequence
C 235	10.6	58.9	27	6	A45806	A45806 Sequence 44	308	10.4	57.8	20	6	AR100497	AR100497 Sequence
C 236	10.6	58.9	27	6	AX003575	AX003575 Sequence 25	309	10.4	57.8	20	6	AR136949	AR136949 Sequence
C 237	10.6	58.9	30	6	A97525	A97525 Sequence	310	10.4	57.8	20	6	AR150152	AR150152 Sequence
C 238	10.6	58.9	30	6	AR048786	AR048786 Sequence	311	10.4	57.8	20	6	AR150304	AR150304 Sequence
C 239	10.6	58.9	30	6	AR097637	AR097637 Sequence	312	10.4	57.8	20	6	AR162585	AR162585 Sequence
C 240	10.6	58.9	30	6	AR103227	AR103227 Sequence	313	10.4	57.8	20	6	AR163917	AR163917 Sequence
C 241	10.6	58.9	30	6	AX287139	AX287139 Sequence	314	10.4	57.8	20	6	AX117238	AX117238 Sequence
C 242	10.6	58.9	30	6	A12895	A12895 Sequence 2	315	10.4	57.8	20	6	AX402890	AX402890 Sequence
C 243	10.6	58.9	30	6	156893	156893 Sequence 2	316	10.4	57.8	20	6	I76950	I76950 Sequence 9
C 244	10.6	58.9	30	6	188163	188163 Sequence 2	317	10.4	57.8	20	6	I76950	I76950 Sequence 9
C 245	10.6	58.9	31	6	AX248490	AX248490 Sequence	318	10.4	57.8	20	6	I81041	I81041 Sequence 9
C 246	10.6	58.9	31	6	AR081874	AR081874 Sequence	319	10.4	57.8	21	6	AR148291	AR148291 Sequence
C 247	10.6	58.9	34	6	I34949	I34949 Sequence 35	320	10.4	57.8	21	6	AX097213	AX097213 Sequence
C 248	10.6	58.9	35	6	AX162532	AX162532 Sequence	321	10.4	57.8	22	6	AX072227	AX072227 Sequence
C 249	10.6	58.9	37	6	AR063476	AR063476 Sequence	322	10.4	57.8	22	6	I26338	I26338 Sequence 30
C 250	10.6	58.9	37	6	I28156	I28156 Sequence 13	323	10.4	57.8	23	6	A27196	A27196 Oligonucleo
C 251	10.6	58.9	38	6	AR058958	AR058958 Sequence	324	10.4	57.8	23	6	A12938	A12938 Synthetic P
C 252	10.6	58.9	38	6	AR105232	AR105232 Sequence	325	10.4	57.8	23	6	AR077342	AR077342 Sequence
C 253	10.6	58.9	38	6	AR119153	AR119153 Sequence	326	10.4	57.8	23	6	AR105708	AR105708 Sequence
C 254	10.6	58.9	38	6	AR123524	AR123524 Sequence	327	10.4	57.8	23	6	AR117962	AR117962 Sequence
C 255	10.6	58.9	38	6	AR138177	AR138177 Sequence	328	10.4	57.8	23	6	AX010544	AX010544 Sequence
C 256	10.6	58.9	38	6	AR176738	AR176738 Sequence	329	10.4	57.8	23	6	AX166704	AX166704 Sequence
C 257	10.6	58.9	38	6	AR198309	AR198309 Sequence	330	10.4	57.8	23	6	AX357137	AX357137 Sequence
C 258	10.6	58.9	38	6	AX470002	AX470002 Sequence	331	10.4	57.8	23	6	AX376781	AX376781 Sequence
C 259	10.6	58.9	40	6	A19014	A19014 Oligonucleo	332	10.4	57.8	23	6	EO9109	EO9109 Synthetic O
C 260	10.6	58.9	41	6	AR061383	AR061383 Sequence	333	10.4	57.8	23	6	I27517	I27517 Sequence 31
C 261	10.6	58.9	41	6	AR108282	AR108282 Sequence	334	10.4	57.8	23	6	I25683	I25683 Sequence 11
C 262	10.6	58.9	41	6	AX404879	AX404879 Sequence	335	10.4	57.8	24	6	AR090687	AR090687 Sequence
C 263	10.6	58.9	41	6	I16239	I16239 Sequence 65	336	10.4	57.8	24	6	AR197722	AR197722 Sequence
C 264	10.6	58.9	41	6	166725	166725 Sequence 65	337	10.4	57.8	24	6	AX445250	AX445250 Sequence
C 265	10.6	58.9	41	6	184819	184819 Sequence 65	338	10.4	57.8	24	6	E25701	E25701 Animal with
C 266	10.6	58.9	42	6	A06938	A06938 F.domesticu	339	10.4	57.8	25	6	AR165844	AR165844 Sequence
C 267	10.6	58.9	42	6	AR011352	AR011352 Sequence	340	10.4	57.8	25	6	AR165845	AR165845 Sequence
C 268	10.6	58.9	42	6	AR061012	AR061012 Sequence	341	10.4	57.8	25	6	AR165845	AR165845 Sequence
C 269	10.6	58.9	42	6	AR061016	AR061016 Sequence	342	10.4	57.8	25	6	AR169623	AR169623 Sequence
C 270	10.6	58.9	42	6	AR079772	AR079772 Sequence	343	10.4	57.8	25	6	AX188494	AX188494 Sequence
C 271	10.6	58.9	42	6	AR081302	AR081302 Sequence	344	10.4	57.8	26	6	AX188430	AX188430 Sequence
C 272	10.6	58.9	42	6	AR170652	AR170652 Sequence	345	10.4	57.8	31	6	AX247968	AX247968 Sequence
C 273	10.6	58.9	42	6	AX018722	AX018722 Sequence	346	10.4	57.8	31	6	AX248003	AX248003 Sequence
C 274	10.6	58.9	42	6	AX018726	AX018726 Sequence	347	10.4	57.8	31	6	AX248159	AX248159 Sequence
C 275	10.6	58.9	42	6	AX418351	AX418351 Sequence	348	10.4	57.8	31	6	AX249255	AX249255 Sequence
C 276	10.6	58.9	44	6	I17990	I17990 Sequence 22	349	10.4	57.8	31	6	AX249675	AX249675 Sequence
C 277	10.6	58.9	44	6	AR002174	AR002174 Sequence	350	10.4	57.8	31	6	BD002343	BD002343 Gene comp
C 278	10.6	58.9	44	6	AX202534	AX202534 Sequence	351	10.4	57.8	35	6	AX188424	AX188424 Sequence
C 279	10.6	58.9	45	6	AR035926	AR035926 Sequence	352	10.4	57.8	35	6	AR057075	AR057075 Sequence
C 280	10.6	58.9	45	6	I20162	I20162 Sequence 11	353	10.4	57.8	36	6	AR095675	AR095675 Sequence
C 281	10.6	58.9	46	6	AX111206	AX111206 Sequence	354	10.4	57.8	36	6	AR114833	AR114833 Sequence
C 282	10.6	58.9	47	6	AR013893	AR013893 Sequence	355	10.4	57.8	37	6	AX092843	AX092843 Sequence
C 283	10.6	58.9	47	6	AR033847	AR033847 Sequence	356	10.4	57.8	38	6	A27205	A27205 Oligonucleo
C 284	10.6	58.9	47	6	AR042507	AR042507 Sequence	357	10.4	57.8	38	6	A33846	A33846 Synthetic P

358	10.4	57.8	38	6	AR046406	AR046406 Sequence	431	10.2	56.7	27	6	AX343652	AX343652 Sequence
359	10.4	57.8	38	6	AR046426	AR046426 Sequence	432	10.2	56.7	28	6	AR089366	AR089366 Sequence
360	10.4	57.8	38	6	AR057835	AR057835 Sequence	433	10.2	56.7	28	6	AR093566	AR093566 Sequence
361	10.4	57.8	38	6	AR115593	AR115593 Sequence	434	10.2	56.7	28	6	AR136052	AR136052 Sequence
362	10.4	57.8	38	6	BD001863	BD001863 Method fo	435	10.2	56.7	28	6	AX282010	AX282010 Sequence
363	10.4	57.8	38	6	I27530	Sequence 44	436	10.2	56.7	28	6	BD007566	BD007566 Process O
364	10.4	57.8	38	6	I53458	Sequence 11	437	10.2	56.7	29	6	AR3793	AR3793 Sequence 4
365	10.4	57.8	38	6	I53478	Sequence 12	438	10.2	56.7	29	6	AR059355	AR059355 Sequence
366	10.4	57.8	40	6	AR125309	Sequence	439	10.2	56.7	29	6	AR071631	AR071631 Sequence
367	10.4	57.8	47	6	AX004826	AX004826 Sequence	440	10.2	56.7	29	6	AX188737	AX188737 Sequence
368	10.4	57.8	50	6	AR088341	Sequence	441	10.2	56.7	29	6	AX188745	AX188745 Sequence
369	10.4	57.8	50	6	AR088342	Sequence	442	10.2	56.7	29	6	E11314	E11314 PCR primer
370	10.4	57.8	50	6	AR117933	Sequence	443	10.2	56.7	29	6	E11315	E11315 PCR primer
371	10.4	57.8	50	6	AR117951	Sequence	444	10.2	56.7	30	6	I52059	I52059 Sequence 1
372	10.2	56.7	16	6	AR154543	Sequence	445	10.2	56.7	30	6	A32442	A32442 p12 cloning
373	10.2	56.7	17	6	AR154547	Sequence	446	10.2	56.7	30	6	AX282016	AX282016 Sequence
374	10.2	56.7	17	6	AR191757	Sequence	447	10.2	56.7	30	6	AX282020	AX282020 Sequence
375	10.2	56.7	18	6	AR98005	Sequence 35	448	10.2	56.7	31	6	AX033342	AX033342 Sequence
376	10.2	56.7	18	6	AR192809	Sequence	449	10.2	56.7	31	6	AX248630	AX248630 Sequence
377	10.2	56.7	19	6	AR086960	Sequence	450	10.2	56.7	31	6	BD002754	BD002754 Gene comp
378	10.2	56.7	19	6	AX179542	Sequence	451	10.2	56.7	31	6	E25833	E25833 Method for
379	10.2	56.7	19	6	AX226036	Sequence	452	10.2	56.7	32	6	A18274	A18274 oligonucleo
380	10.2	56.7	19	6	AX226037	Sequence	453	10.2	56.7	32	6	AR069600	AR069600 Sequence
381	10.2	56.7	19	6	I84460	Sequence 1	454	10.2	56.7	32	6	AR069603	AR069603 Sequence
382	10.2	56.7	20	6	A36292	Sequence 15	455	10.2	56.7	32	6	AX188719	AX188719 Sequence
383	10.2	56.7	20	6	AR062664	Sequence	456	10.2	56.7	32	6	AX306632	AX306632 Sequence
384	10.2	56.7	20	6	AR104767	Sequence	457	10.2	56.7	32	6	I15742	I15742 Sequence 8
385	10.2	56.7	20	6	AR105589	Sequence	458	10.2	56.7	33	6	AR152548	AR152548 Sequence
386	10.2	56.7	20	6	AR121074	Sequence	459	10.2	56.7	33	6	AX031406	AX031406 Sequence
387	10.2	56.7	20	6	AR123251	Sequence	460	10.2	56.7	33	6	I31032	I31032 Sequence 64
388	10.2	56.7	20	6	AR162355	Sequence	461	10.2	56.7	33	13	AX031516	AX031516 Sequence
389	10.2	56.7	20	6	AR211292	Sequence	462	10.2	56.7	34	6	AR073546	AR073546 Sequence
390	10.2	56.7	20	6	AX076196	Sequence	463	10.2	56.7	34	6	AX033207	AX033207 Sequence
391	10.2	56.7	20	6	AX194390	Sequence	464	10.2	56.7	34	6	I20488	I20488 Sequence 10
392	10.2	56.7	20	6	AX293085	Sequence	465	10.2	56.7	36	6	AR136044	AR136044 Sequence
393	10.2	56.7	20	6	AX294251	Sequence	466	10.2	56.7	36	6	AR136069	AR136069 Sequence
394	10.2	56.7	20	6	AX296272	Sequence	467	10.2	56.7	36	6	AR203924	AR203924 Sequence
395	10.2	56.7	20	6	AX371349	Sequence	468	10.2	56.7	36	6	AX049403	AX049403 Sequence
396	10.2	56.7	20	6	AX403130	Sequence	469	10.2	56.7	36	6	AX053075	AX053075 Sequence
397	10.2	56.7	20	6	AX453030	Sequence	470	10.2	56.7	36	6	AX085425	AX085425 Sequence
398	10.2	56.7	20	6	BD011252	BD011252 Human tel	471	10.2	56.7	36	6	AX268692	AX268692 Sequence
399	10.2	56.7	20	6	E37001	E37001 Human telom	472	10.2	56.7	36	6	BD007558	BD007558 Process O
400	10.2	56.7	20	6	I20666	Sequence 64	473	10.2	56.7	36	6	BD007583	BD007583 Process O
401	10.2	56.7	20	6	I33359	Sequence 64	474	10.2	56.7	37	6	AR048870	AR048870 Sequence
402	10.2	56.7	20	6	I83392	Sequence 15	475	10.2	56.7	38	6	AX378841	AX378841 Sequence
403	10.2	56.7	21	6	AR091658	Sequence	476	10.2	56.7	38	6	AX378842	AX378842 Sequence
404	10.2	56.7	21	6	AR137952	Sequence	477	10.2	56.7	40	6	AR149456	AR149456 Sequence
405	10.2	56.7	21	6	AX095232	Sequence	478	10.2	56.7	40	6	AX356280	AX356280 Sequence
406	10.2	56.7	21	6	AX095687	Sequence	479	10.2	56.7	40	6	E94928	E94928 Method for
407	10.2	56.7	21	6	AX322557	Sequence	480	10.2	56.7	41	6	BD009289	BD009289 Mutant pe
408	10.2	56.7	22	6	I81383	Sequence 9	481	10.2	56.7	42	6	AX085431	AX085431 Sequence
409	10.2	56.7	23	6	A62922	Sequence 16	482	10.2	56.7	43	6	A05113	A05113 Oligonucleo
410	10.2	56.7	23	6	AX088725	Sequence	483	10.2	56.7	44	6	I38535	I38535 Sequence 3
411	10.2	56.7	23	6	AX088726	Sequence	484	10.2	56.7	44	9	HMSPARC01	M27537 Human ostreo
412	10.2	56.7	24	6	AR175963	Sequence	485	10.2	56.7	45	6	AX201009	AX201009 Sequence
413	10.2	56.7	24	6	AX098725	Sequence	486	10.2	56.7	45	6	AX267808	AX267808 Sequence
414	10.2	56.7	24	6	AX136953	Sequence	487	10.2	56.7	45	6	I26650	I26650 Sequence 17
415	10.2	56.7	24	6	AX288452	Sequence	488	10.2	56.7	50	1	PSECLPBA	L06014 Pseudomonas
416	10.2	56.7	24	6	AX289618	Sequence	489	10.2	56.7	50	6	AX159966	AX159966 Sequence
417	10.2	56.7	24	6	AX291639	Sequence	490	10.2	56.7	14	6	E12333	E12333 Primer 4/1
418	10.2	56.7	25	6	AR003574	Sequence	491	10.2	56.7	16	6	I33376	I33376 Sequence 34
419	10.2	56.7	25	6	AR075590	Sequence	492	10.2	56.7	17	6	AX356583	AX356583 Sequence
420	10.2	56.7	25	6	AR082293	Sequence	493	10.2	56.7	17	6	AX362565	AX362565 Sequence
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425	10.2	56.7	27	6	A08050	Oligonucleo	498	10.2	56.7	19	6	AR205714	AR205714 Sequence
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509	10	55.6	20	12	AB068545	AB068545 Synthetic	c 582	10	55.6	33	6	AR067682	AR067682 Sequence
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c 511	10	55.6	21	6	AR020910	AR020910 Sequence	c 584	10	55.6	33	6	AX059024	AX059024 Sequence
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c 513	10	55.6	21	6	AX095342	AX095342 Sequence	c 586	10	55.6	33	10	MMTCRVJAL	222840 M. musculus
c 514	10	55.6	21	6	AX095353	AX095353 Sequence	c 587	10	55.6	35	6	AX008754	AX008754 Sequence
c 515	10	55.6	21	6	AX095407	AX095407 Sequence	c 588	10	55.6	35	6	AX192339	AX192339 Sequence
c 516	10	55.6	21	6	AX097158	AX097158 Sequence	c 589	10	55.6	35	6	BD000574	BD000574 Human pol
c 517	10	55.6	22	10	AX154443	AX154443 Sequence	c 590	10	55.6	36	6	AR068332	AR068332 Sequence
c 518	10	55.6	22	10	MMTC1902A	249042 M. musculus	c 591	10	55.6	36	6	AR178394	AR178394 Sequence
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c 520	10	55.6	23	6	AR197570	AR197570 Sequence	c 593	10	55.6	36	6	AX220152	AX220152 Sequence
c 521	10	55.6	23	6	AX287628	AX287628 Sequence	c 594	10	55.6	39	6	AR031982	AR031982 Sequence
c 522	10	55.6	23	6	AX300573	AX300573 Sequence	c 595	10	55.6	40	6	AR062591	AR062591 Sequence
c 523	10	55.6	23	6	AX477190	AX477190 Sequence	c 596	10	55.6	40	6	AR206819	AR206819 Sequence
c 524	10	55.6	24	6	AR086083	AR086083 Sequence	c 597	10	55.6	40	6	AR206821	AR206821 Sequence
c 525	10	55.6	24	6	AR109796	AR109796 Sequence	c 598	10	55.6	40	6	AR206823	AR206823 Sequence
c 526	10	55.6	24	6	AR112021	AR112021 Sequence	c 599	10	55.6	40	6	115913	115913 Sequence 14
c 527	10	55.6	24	6	AR140437	AR140437 Sequence	c 600	10	55.6	40	6	196112	196112 Sequence 14
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c 530	10	55.6	24	6	AX288860	AX288860 Sequence	c 603	10	55.6	42	6	AX045349	AX045349 Sequence
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c 532	10	55.6	24	6	AX403564	AX403564 Sequence	c 605	10	55.6	43	6	AR013755	AR013755 Sequence
c 533	10	55.6	25	6	122152	122152 Sequence 11	c 606	10	55.6	43	14	D88714	D88714 Hepatitis G
c 534	10	55.6	25	6	A91508	A91508 Sequence 35	c 607	10	55.6	43	14	D88720	D88720 Hepatitis G
c 535	10	55.6	25	6	AX042486	AX042486 Sequence	c 608	10	55.6	44	6	A13023	A13023 Partial HBV
c 536	10	55.6	25	6	AX476046	AX476046 Sequence	c 609	10	55.6	45	9	HSB3VB3	X84272 H. sapiens m
c 537	10	55.6	25	6	AX476047	AX476047 Sequence	c 610	10	55.6	45	9	HSB3VB3	269506 H. sapiens m
c 538	10	55.6	25	6	AX476048	AX476048 Sequence	c 611	10	55.6	45	9	HSB3VB3	269506 H. sapiens m
c 539	10	55.6	25	6	AX476049	AX476049 Sequence	c 612	10	55.6	48	6	AR011227	AR011227 Sequence
c 540	10	55.6	25	6	AX476050	AX476050 Sequence	c 613	10	55.6	48	6	AR076511	AR076511 Sequence
c 541	10	55.6	25	6	AX476051	AX476051 Sequence	c 614	10	55.6	48	6	AR167302	AR167302 Sequence
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c 544	10	55.6	25	10	MMTC11X42	249020 M. musculus	c 617	10	55.6	48	6	E16432	E16432 DNA encodin
c 545	10	55.6	26	6	AR142098	AR142098 Sequence	c 618	10	55.6	48	6	117865	117865 Sequence 95
c 546	10	55.6	26	6	AR151423	AR151423 Sequence	c 619	10	55.6	48	6	145981	145981 Sequence 5
c 547	10	55.6	26	6	AR157416	AR157416 Sequence	c 620	10	55.6	48	9	AX026057	AX026057 Sequence
c 548	10	55.6	26	6	AX033900	AX033900 Sequence	c 621	10	55.6	49	6	AX026057	AX026057 Sequence
c 549	10	55.6	26	6	AX045707	AX045707 Sequence	c 622	10	55.6	49	6	106908	106908 Sequence 3
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c 551	10	55.6	26	6	AX374667	AX374667 Sequence	c 624	10	55.6	50	6	AR125775	AR125775 Sequence
c 552	10	55.6	26	10	MMTCUR94	249039 M. musculus	c 625	10	55.6	50	6	AR166926	AR166926 Sequence
c 553	10	55.6	27	6	AR109750	AR109750 Sequence	c 626	10	55.6	50	6	AX199420	AX199420 Sequence
c 554	10	55.6	27	6	AX049980	AX049980 Sequence	c 627	10	55.6	50	6	AX199422	AX199422 Sequence
c 555	10	55.6	27	6	E04885	E04885 Synthetic D	c 628	10	55.6	50	6	AX199586	AX199586 Sequence
c 556	10	55.6	27	10	MMM1314	X94907 M. musculus	c 629	10	55.6	50	6	147187	147187 Sequence 11
c 557	10	55.6	28	6	AR124803	AR124803 Sequence	c 630	10	55.6	50	10	AF071703	AF071703 Mus muscu
c 558	10	55.6	28	6	AX098012	AX098012 Sequence	c 631	9.8	54.4	13	6	AX304729	AX304729 Sequence
c 559	10	55.6	28	6	189924	189924 Sequence 8	c 632	9.8	54.4	13	6	AX304862	AX304862 Sequence
c 560	10	55.6	28	9	S78962	S78962 T-cell rece	c 633	9.8	54.4	16	6	AX304730	AX304730 Sequence
c 561	10	55.6	29	6	AR109231	AR109231 Sequence	c 634	9.8	54.4	16	6	AX304863	AX304863 Sequence
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c 563	10	55.6	29	6	BD001054	BD001054 Method an	c 636	9.8	54.4	17	6	AR190315	AR190315 Sequence
c 564	10	55.6	29	6	BD001055	BD001055 Method an	c 637	9.8	54.4	17	6	AR190543	AR190543 Sequence
c 565	10	55.6	29	6	BD001483	BD001483 Method an	c 638	9.8	54.4	17	6	AX215072	AX215072 Sequence
c 566	10	55.6	29	6	BD001484	BD001484 Method an	c 639	9.8	54.4	17	6	AX215073	AX215073 Sequence
c 567	10	55.6	29	6	103859	103859 Sequence 16	c 640	9.8	54.4	17	6	AX215935	AX215935 Sequence
c 568	10	55.6	30	6	AR036161	AR036161 Sequence	c 641	9.8	54.4	17	6	AX215936	AX215936 Sequence
c 569	10	55.6	30	6	AR048719	AR048719 Sequence	c 642	9.8	54.4	17	6	AX215937	AX215937 Sequence
c 570	10	55.6	30	6	AR125760	AR125760 Sequence	c 643	9.8	54.4	17	6	AX422860	AX422860 Sequence
c 571	10	55.6	30	6	AX192395	AX192395 Sequence	c 644	9.8	54.4	17	6	AX422861	AX422861 Sequence
c 572	10	55.6	30	6	BD000570	BD000570 Human pol	c 645	9.8	54.4	17	6	AX475064	AX475064 Sequence
c 573	10	55.6	30	6	100877	100877 Sequence 7	c 646	9.8	54.4	17	6	AX475065	AX475065 Sequence
c 574	10	55.6	30	6	104521	104521 Sequence 14	c 647	9.8	54.4	17	6	AX475066	AX475066 Sequence
c 575	10	55.6	30	6	147172	147172 Sequence 10	c 648	9.8	54.4	17	6	AX475067	AX475067 Sequence
c 576	10	55.6	31	6	AX109247	AX109247 Sequence	c 649	9.8	54.4	17	6	AX475068	AX475068 Sequence

650	9.8	54.4	18	6	AR096345	AR096345 Sequence	c 723	9.8	54.4	24	6	AX444384	AX444384 Sequence
651	9.8	54.4	18	6	AR096346	AR096346 Sequence	724	9.8	54.4	24	6	AX445085	AX445085 Sequence
652	9.8	54.4	18	6	AR102978	AR102978 Sequence	725	9.8	54.4	24	6	AX445284	AX445284 Sequence
653	9.8	54.4	18	6	AR117373	AR117373 Sequence	726	9.8	54.4	24	6	AX447217	AX447217 Sequence
654	9.8	54.4	18	6	AR117374	AR117374 Sequence	727	9.8	54.4	25	6	AR137546	AR137546 Sequence
655	9.8	54.4	18	6	AR134127	AR134127 Sequence	728	9.8	54.4	25	6	AR139052	AR139052 Sequence
656	9.8	54.4	18	6	AR134128	AR134128 Sequence	729	9.8	54.4	25	6	AX042470	AX042470 Sequence
657	9.8	54.4	18	6	AR160826	AR160826 Sequence	730	9.8	54.4	25	6	AX080324	AX080324 Sequence
658	9.8	54.4	18	6	AR190758	AR190758 Sequence	731	9.8	54.4	25	6	AX115810	AX115810 Sequence
659	9.8	54.4	18	6	AR205152	AR205152 Sequence	732	9.8	54.4	25	6	AX196855	AX196855 Sequence
660	9.8	54.4	18	6	AR205153	AR205153 Sequence	733	9.8	54.4	25	6	AX281131	AX281131 Sequence
661	9.8	54.4	18	6	AX278608	AX278608 Sequence	734	9.8	54.4	25	6	AX476041	AX476041 Sequence
662	9.8	54.4	18	6	AX299455	AX299455 Sequence	735	9.8	54.4	25	6	AX476042	AX476042 Sequence
663	9.8	54.4	18	6	124705	124705 Sequence 9	736	9.8	54.4	25	6	AX476043	AX476043 Sequence
664	9.8	54.4	18	6	128106	128106 Sequence 27	737	9.8	54.4	25	6	AX476044	AX476044 Sequence
665	9.8	54.4	19	6	AR035651	AR035651 Sequence	738	9.8	54.4	25	6	AX476045	AX476045 Sequence
666	9.8	54.4	19	6	AR152860	AR152860 Sequence	739	9.8	54.4	26	6	A12855	A12855 Oligonucleo
667	9.8	54.4	19	6	AR158133	AR158133 Sequence	740	9.8	54.4	26	6	AR086576	AR086576 Sequence
668	9.8	54.4	19	6	AR174299	AR174299 Sequence	741	9.8	54.4	26	6	AR208612	AR208612 Sequence
669	9.8	54.4	19	6	AR179745	AR179745 Sequence	742	9.8	54.4	26	6	AR037849	AR037849 Sequence
670	9.8	54.4	19	6	AX128943	AX128943 Sequence	743	9.8	54.4	26	6	AX080327	AX080327 Sequence
671	9.8	54.4	19	6	AX129094	AX129094 Sequence	744	9.8	54.4	26	6	AX135842	AX135842 Sequence
672	9.8	54.4	19	6	AX130668	AX130668 Sequence	745	9.8	54.4	26	6	AX196922	AX196922 Sequence
673	9.8	54.4	19	6	AX304731	AX304731 Sequence	746	9.8	54.4	27	6	AR4247	AR4247 Sequence 14
674	9.8	54.4	19	6	AX304864	AX304864 Sequence	747	9.8	54.4	27	6	AR039462	AR039462 Sequence
675	9.8	54.4	19	6	E10733	E10733 Primer for	748	9.8	54.4	27	6	AR040046	AR040046 Sequence
676	9.8	54.4	19	6	128105	128105 Sequence 27	749	9.8	54.4	27	6	AR040424	AR040424 Sequence
677	9.8	54.4	19	6	140842	140842 Sequence 11	750	9.8	54.4	27	6	AR177836	AR177836 Sequence
678	9.8	54.4	19	6	178495	178495 Sequence 6	751	9.8	54.4	27	6	AR190813	AR190813 Sequence
679	9.8	54.4	19	11	HUM265UYA	DS0161 A PCR prime	752	9.8	54.4	27	6	AX058645	AX058645 Sequence
680	9.8	54.4	20	6	AR009309	AR009309 Sequence	753	9.8	54.4	27	6	AX117248	AX117248 Sequence
681	9.8	54.4	20	6	AR009361	AR009361 Sequence	754	9.8	54.4	28	6	AS0947	AS0947 Sequence 26
682	9.8	54.4	20	6	AR026499	AR026499 Sequence	755	9.8	54.4	28	6	AR072784	AR072784 Sequence
683	9.8	54.4	20	6	AR095025	AR095025 Sequence	756	9.8	54.4	28	6	AR090426	AR090426 Sequence
684	9.8	54.4	20	6	AR136000	AR136000 Sequence	757	9.8	54.4	28	6	AR197461	AR197461 Sequence
685	9.8	54.4	20	6	AR194802	AR194802 Sequence	758	9.8	54.4	29	6	AX000647	AX000647 Sequence
686	9.8	54.4	20	6	AX076269	AX076269 Sequence	759	9.8	54.4	29	6	AX000651	AX000651 Sequence
687	9.8	54.4	20	6	AX076270	AX076270 Sequence	760	9.8	54.4	29	6	AX000652	AX000652 Sequence
688	9.8	54.4	20	6	AX149032	AX149032 Sequence	761	9.8	54.4	29	6	AX021170	AX021170 Sequence
689	9.8	54.4	20	6	AX326875	AX326875 Sequence	762	9.8	54.4	30	6	AR030429	AR030429 Sequence
690	9.8	54.4	20	6	BD002077	BD002077 Detection	763	9.8	54.4	30	6	AR052864	AR052864 Sequence
691	9.8	54.4	20	6	E37099	E37099 Method for	764	9.8	54.4	30	6	AR176617	AR176617 Sequence
692	9.8	54.4	20	6	E63428	E63428 Method for	765	9.8	54.4	30	6	AX000653	AX000653 Sequence
693	9.8	54.4	20	6	E63444	E63444 Method for	766	9.8	54.4	30	6	AX428463	AX428463 Sequence
694	9.8	54.4	21	6	A63960	A63960 Sequence 4	767	9.8	54.4	30	6	AX428495	AX428495 Sequence
695	9.8	54.4	21	6	A91533	A91533 Sequence 60	768	9.8	54.4	30	6	115727	115727 Sequence 2
696	9.8	54.4	21	6	A98267	A98267 Sequence 20	769	9.8	54.4	31	6	AR147746	AR147746 Sequence
697	9.8	54.4	21	6	AR060269	AR060269 Sequence	770	9.8	54.4	31	6	AR159768	AR159768 Sequence
698	9.8	54.4	21	6	AR091470	AR091470 Sequence	771	9.8	54.4	31	6	AR160460	AR160460 Sequence
699	9.8	54.4	21	6	AX235879	AX235879 Sequence	772	9.8	54.4	31	6	AR195804	AR195804 Sequence
700	9.8	54.4	21	6	E35272	E35272 Hybridoma C	773	9.8	54.4	31	6	AR199699	AR199699 Sequence
701	9.8	54.4	22	6	AR003452	AR003452 Sequence	774	9.8	54.4	31	6	AR202416	AR202416 Sequence
702	9.8	54.4	22	6	AX099230	AX099230 Sequence	775	9.8	54.4	31	6	AX221118	AX221118 Sequence
703	9.8	54.4	22	6	AX210201	AX210201 Sequence	776	9.8	54.4	31	6	AX248151	AX248151 Sequence
704	9.8	54.4	22	6	AX487085	AX487085 Sequence	777	9.8	54.4	31	6	AX248152	AX248152 Sequence
705	9.8	54.4	23	6	A31977	A31977 Synthetic H	778	9.8	54.4	31	6	AX248332	AX248332 Sequence
706	9.8	54.4	23	6	AR003443	AR003443 Sequence	779	9.8	54.4	31	6	AX249254	AX249254 Sequence
707	9.8	54.4	23	6	AR089639	AR089639 Sequence	780	9.8	54.4	31	6	AX249322	AX249322 Sequence
708	9.8	54.4	23	6	AR131396	AR131396 Sequence	781	9.8	54.4	31	6	AX280064	AX280064 Sequence
709	9.8	54.4	23	6	AX202165	AX202165 Sequence	782	9.8	54.4	31	6	AX425786	AX425786 Sequence
710	9.8	54.4	23	6	AX370819	AX370819 Sequence	783	9.8	54.4	31	6	BD002805	BD002805 Gene comp
711	9.8	54.4	23	6	BD001801	BD001801 Immunogen	784	9.8	54.4	32	6	A70841	A70841 Sequence 8
712	9.8	54.4	24	6	A61979	A61979 Sequence 9	785	9.8	54.4	32	6	AR176621	AR176621 Sequence
713	9.8	54.4	24	6	AR090844	AR090844 Sequence	786	9.8	54.4	32	6	AR208154	AR208154 Sequence
714	9.8	54.4	24	6	AR177814	AR177814 Sequence	787	9.8	54.4	32	6	AX025107	AX025107 Sequence
715	9.8	54.4	24	6	AR197879	AR197879 Sequence	788	9.8	54.4	32	6	AX174814	AX174814 Sequence
716	9.8	54.4	24	6	AX061528	AX061528 Sequence	789	9.8	54.4	33	6	AR004403	AR004403 Sequence
717	9.8	54.4	24	6	AX154933	AX154933 Sequence	790	9.8	54.4	33	6	AR064942	AR064942 Sequence
718	9.8	54.4	24	6	AX288860	AX288860 Sequence	791	9.8	54.4	33	6	AR097195	AR097195 Sequence
719	9.8	54.4	24	6	AX292370	AX292370 Sequence	792	9.8	54.4	33	6	AR130693	AR130693 Sequence
720	9.8	54.4	24	6	AX329548	AX329548 Sequence	793	9.8	54.4	33	6	AR172042	AR172042 Sequence
721	9.8	54.4	24	6	AX350849	AX350849 Sequence	794	9.8	54.4	33	6	E38623	E38623 Method for
722	9.8	54.4	24	6	AX419033	AX419033 Sequence	795	9.8	54.4	33	6	182878	182878 Sequence 57

796	9.8	54.4	35	6	A47109	Sequence	2																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
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942	9.6	53.3	24	6	E30488
943	9.6	53.3	24	23	BD008279
944	9.6	53.3	25	6	AA2060
945	9.6	53.3	25	6	ARI58390
946	9.6	53.3	25	6	ARI58391
947	9.6	53.3	25	6	ARI58392
948	9.6	53.3	25	6	ARI58393
949	9.6	53.3	25	6	ARI58394
950	9.6	53.3	25	6	ARI58395
951	9.6	53.3	25	6	ARI58396
952	9.6	53.3	25	6	ARI58397
953	9.6	53.3	25	6	ARI58398
954	9.6	53.3	25	6	ARI58399
955	9.6	53.3	25	6	AX038540
956	9.6	53.3	25	6	AX060480
957	9.6	53.3	25	6	BD005978
958	9.6	53.3	25	6	BD005985
959	9.6	53.3	25	6	BD005992
960	9.6	53.3	26	6	AX033455
961	9.6	53.3	26	6	AX365257
962	9.6	53.3	26	6	BD010752
963	9.6	53.3	26	6	E30993
964	9.6	53.3	27	6	AA1158
965	9.6	53.3	27	6	AR030385
966	9.6	53.3	27	6	AR143813
967	9.6	53.3	27	6	AX203570
968	9.6	53.3	27	6	AX278552
969	9.6	53.3	27	6	AX280685
970	9.6	53.3	27	6	AX418361
971	9.6	53.3	27	6	AX418385
972	9.6	53.3	28	6	AA0665
973	9.6	53.3	28	6	AR148899
974	9.6	53.3	28	6	AX031643
975	9.6	53.3	28	6	AX031913
976	9.6	53.3	28	6	AX032183
977	9.6	53.3	28	6	AX319390
978	9.6	53.3	29	6	AA06418
979	9.6	53.3	29	6	AA10237
980	9.6	53.3	29	6	AA3384
981	9.6	53.3	29	6	AR035539
982	9.6	53.3	29	6	AR081876
983	9.6	53.3	29	6	AR093163
984	9.6	53.3	29	6	AX038844
985	9.6	53.3	29	6	AX440317
986	9.6	53.3	30	6	E11459
987	9.6	53.3	30	6	AR048682
988	9.6	53.3	30	6	AR093165
989	9.6	53.3	30	6	AR116796
990	9.6	53.3	30	6	AX058064
991	9.6	53.3	30	6	AX081615
992	9.6	53.3	30	6	AX374796
993	9.6	53.3	31	6	AX247988
994	9.6	53.3	31	6	AX249059
995	9.6	53.3	31	6	AX249195
996	9.6	53.3	31	6	AX249253
997	9.6	53.3	31	6	E11401
998	9.6	53.3	32	6	AA3385
999	9.6	53.3	32	6	AR059492
1000	9.6	53.3	32	6	ARI56441

ALIGNMENTS

RESULT 1
LOCUS AX298039 18 bp DNA
DEFINITION Sequence 35 from Patent WO0183740.
ACCESSION AX298039
VERSION AX298039.1 GI:17128125
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.

REFERENCE 1 artificial sequences.

AUTHORS Iversen, P. L. and Hudziak, R.

TITLE Splice-region antisense composition and method

JOURNAL Patent: WO 0183740-A 35 08-NOV-2001;

Avi Biopharma, Inc. (US)

FEATURES Location/Qualifiers

source

1..18

BASE COUNT 3 a 6 c 7 g 2 t

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18

Db 1 CCCGGAAGCAGCTGGC 18

RESULT 2
LOCUS AX298040 36 bp DNA
DEFINITION Sequence 36 from Patent WO0183740.
ACCESSION AX298040
VERSION AX298040.1 GI:17128126

KEYWORDS
SOURCE synthetic construct.

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Iversen, P. L. and Hudziak, R.

TITLE Splice-region antisense composition and method

JOURNAL Patent: WO 0183740-A 36 08-NOV-2001;

Avi Biopharma, Inc. (US)

FEATURES Location/Qualifiers

1..36

BASE COUNT 6 a 11 c 12 g 7 t

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 36;

Best Local Similarity 100.0%; Pred. No. 6.9e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18

Db 17 CCCGGAAGCAGCTGGC 34

RESULT 3

LOCUS I06689

DEFINITION Sequence 2 from Patent WO 9009180. 28 bp DNA
ACCESSION I06689

VERSION I06689.1 GI:589476

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)

AUTHORS Smith, L.J. and A61K31.

TITLE METHODS AND COMPOSITIONS FOR TREATMENT OF CANCER USING

OLIGONUCLEOTIDES

JOURNAL Patent: WO 9009180-A 2 23-AUG-1990;

FEATURES Location/Qualifiers

source

1..28

/organism="unknown"

BASE COUNT 4 a 11 c 7 g 6 t
ORIGIN
Query Match 94.4%; Score 17; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCGAGGAGCTCTGG 17
Db 17 CCCGAGGAGCTCTGG 1

RESULT 4
LOCUS AR003360/c 25 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 7 from patent US 5744303.
ACCESSION AR003360
VERSION AR003360.1 GI:3964619
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS 1990.R., Friend,S.H., Frebourg,T. and Ishioka,C.
TITLE Functional assay for transcriptional regulator genes
JOURNAL Patent: US 5744303-A 7 28-APR-1998;
FEATURES
source Location/Qualifiers
1..25
/organism="unknown"
BASE COUNT 4 a 8 c 7 g 6 t
ORIGIN

Query Match 83.3%; Score 15; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 GGAAGGAGCTCTGGC 18
Db 25 GGAAGGAGCTCTGGC 11

RESULT 5
LOCUS AX053071/c 26 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 3 from Patent W00071078.
ACCESSION AX053071
VERSION AX053071.1 GI:12227129
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Ehts,P. and Jund,R.
TITLE Composition designed for implementing an antitumoral or antiviral
JOURNAL treatment in a mammal
TRANSGENE S.A. (FR)
FEATURES
source Location/Qualifiers
1..26
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="amorce"
BASE COUNT 5 a 9 c 7 g 5 t
ORIGIN

Query Match 82.2%; Score 14.8; DB 6; Length 26;
Best Local Similarity 88.9%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CCCGAGGAGCTCTGGC 18
Db 22 CCCGAGGAGCTCTGGC 5

RESULT 6
LOCUS AX464857 21 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 8 from Patent W00212463.
ACCESSION AX464857
VERSION AX464857.1 GI:21899557
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gualfetti,P., Mitchinson,C. and Ropp,T.H.
TITLE Mutant EgII cellulase, DNA encoding such
JOURNAL methods for obtaining same
Patent: WO 0212463-A 8 14-FEB-2002;
GENECOR INTERNATIONAL, INC. (US)
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 3 a 8 c 7 g 3 t
ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CCCGAGGAGCTCTGGC 18
Db 4 CCTGGAGGAGCTCTGGC 21

RESULT 7
LOCUS AX464856 27 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 7 from Patent W00212463.
ACCESSION AX464856
VERSION AX464856.1 GI:21899556
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gualfetti,P., Mitchinson,C. and Ropp,T.H.
TITLE Mutant EgII cellulase, DNA encoding such EgII compositions and
JOURNAL methods for obtaining same
Patent: WO 0212463-A 7 14-FEB-2002;
GENECOR INTERNATIONAL, INC. (US)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 3 a 10 c 11 g 3 t
ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 27;
Best Local Similarity 83.3%; Pred. No. 1.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CCCGAGGAGCTCTGGC 18
Db 21 CCTGGAGGAGCTCTGGC 4

RESULT 8
LOCUS AR137946 26 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 22 from patent US 6197580.
ACCESSION AR137946
VERSION AR137946.1 GI:14479455

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Susulic,V.S. and Duzic,E.
TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor gene
JOURNAL Patent: US 6197580-A 22-06-MAR-2001;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"
BASE COUNT 3 a 11 c 5 g 7 t
ORIGIN

Query Match 68.9%; Score 12.4; DB 6; Length 26;
Best Local Similarity 92.9%; Pred. No. 4.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GAAGCAGCTGTGGC 18
DB 24 GAAGCAGCTGTGGC 11

RESULT 9
LOCUS AX348011/c 17 bp DNA linear PAT 06-PEB-2002
DEFINITION Sequence 44 from Patent EP1172444.
ACCESSION AX348011
VERSION AX348011.1 GI:18614121
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Schreiber,S., Hampe,J. and Mascheretti,S.
TITLE Diagnostic use of polymorphisms in the gene coding for the tnfr receptor II and method for detecting non-responders to anti-tnf therapy
JOURNAL Patent: EP 1172444-A 44-16-JAN-2002;
FEATURES Conaris Research Institute GmbH (DE)
source Location/Qualifiers
1..17
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Reverse Primer"
BASE COUNT 3 a 8 c 4 g 2 t
ORIGIN

Query Match 67.8%; Score 12.2; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCGGAGGCGACTGTGG 17
DB 17 CCGGAGGCGCTGTGG 1

RESULT 10
LOCUS AR174377/c 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 37 from patent US 6306655.
ACCESSION AR174377
VERSION AR174377.1 GI:17914697
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP alpha expression
JOURNAL Patent: US 6306655-A 37-23-OCT-2001;
FEATURES Location/Qualifiers

source 1..20
/organism="unknown"
BASE COUNT 3 a 8 c 6 g 3 t
ORIGIN

Query Match 67.8%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCGGAGGCGACTGTGG 17
DB 17 CCGGAGGCGAGCTGTGG 1

RESULT 11
LOCUS E10818 23 bp DNA linear PAT 29-SEP-1997
DEFINITION FITC labelling sequencing primer for detecting cellulose from Humicola insolens.
ACCESSION E10818
VERSION E10818.1 GI:22027913
KEYWORDS JP 1996056663-A/8.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Watanabe,M., Sumida,N., Kawabata,K., Aoyanagi,K., Hamaya,T., Hirayama,M. and Murakami,T.
TITLE NEW CELLULOSE AND ITS GENE
JOURNAL Patent: JP 1996056663-A 8-05-MAR-1996;
COMMENT MEIJI SEIKA KAISHA LTD
OS None
OC Artificial sequences.
PN JP 1996056663-A/8
PD 05-MAR-1996
PF 29-AUG-1994 JP 1994203564
PI WATANABE MANABU, SUMIDA NAOMI, KAWABATA KEIKO, AOYANAGI KAORU, HAMAYA TORU, HIRAYAMA MASAO, MURAKAMI TAKESHI PC
C12N9/42.C12N15/09.(C12N9/42.C12R1:19);
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
FH key Location/Qualifiers
FT source 1..23
/organism="Artificial sequences" FT
misc_feature 1..23 /note="Primer,WATA-11".

FEATURES
source Location/Qualifiers
1..23
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 6 a 5 c 8 g 4 t
ORIGIN

Query Match 67.8%; Score 12.2; DB 6; Length 23;
Best Local Similarity 82.4%; Pred. No. 5.6e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CCGGAGGCGACTGTGGC 18
DB 3 CCGGAGGAGAAATCTTGC 19

RESULT 12
LOCUS AR066373 26 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5849994.
ACCESSION AR066373
VERSION AR066373.1 GI:5996589
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

```
Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Narayan,O.
TITLE Animal model for HIV-1 induced disease
JOURNAL Patent: US 5849994-A 12 15-DEC-1998;
FEATURES
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        1. .26
            /organism="unknown"
BASE COUNT      8 a      5 c      11 g      2 t
ORIGIN
Query Match
Best Local Similarity 82.4%; Score 12.2; DB 6; Length 26;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCGGAGGCAAGCTGGC 17
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    1 CCGGAGGCAAGCTGGC 17
Db 1 CCGGAGGCAAGCTGGC 17

RESULT 13
AX004559
LOCUS AX004559 33 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 11 from Patent WO915684.
ACCESSION AX004559
VERSION AX004559.1 GI:9927999
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct.
        artificial sequences.
REFERENCE 1 (bases 1 to 33)
AUTHORS Binley,K.M. and Naylor,S.
TITLE Patent: WO 9915684-A 11 01-APR-1999;
JOURNAL BINFLEY KATIE MARY (GB); OXFORD BIOMEDICA UK LIMITED (GB)
FEATURES
    source
        1. .33
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="synthetic oligonucleotide"
BASE COUNT      10 a      11 c      9 g      3 t
ORIGIN
Query Match
Best Local Similarity 82.4%; Score 12.2; DB 6; Length 33;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGGAGGCAAGCTGGC 18
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    1 CCGGAGGCAAGCTGGC 18
Db 7 CCGGAGGCAAGCTGGC 23

RESULT 14
AX004579
LOCUS AX004579 33 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 11 from Patent WO915683.
ACCESSION AX004579
VERSION AX004579.1 GI:9928019
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct.
        artificial sequences.
REFERENCE 1 (bases 1 to 33)
AUTHORS Kingsman,A. and Uden,M.
TITLE Retroviral vectors comprising a functional splice donor site and a
JOURNAL functional splice acceptor site
PATENT: WO 9915683-A 11 01-APR-1999;
OXFORD BIOMEDICA UK LIMITED (GB); KINGSMAN ALAN (GB)
FEATURES
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        1. .33
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="synthetic oligonucleotide"

BASE COUNT      10 a      11 c      9 g      3 t
ORIGIN
Query Match
Best Local Similarity 82.4%; Score 12.2; DB 6; Length 33;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGGAGGCAAGCTGGC 18
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    1 CCGGAGGCAAGCTGGC 18
Db 7 CCGGAGGCAAGCTGGC 23

RESULT 15
AX036650
LOCUS AX036650 33 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 11 from Patent WO0056910.
ACCESSION AX036650
VERSION AX036650.1 GI:1126225
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct.
        artificial sequences.
REFERENCE 1 (bases 1 to 33)
AUTHORS Mitropoulos,K. and Uden,M.
TITLE Retroviral vectors comprising functional and non-functional splice
JOURNAL donor and splice acceptor sites
PATENT: WO 0056910-A 11 28-SEP-2000.
MITROPHOLOS KYRIACOS (GB); UDEN MARK (GB); OXFORD BIOMEDICA LTD
(GB)
FEATURES
    source
        1. .33
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="synthetic oligonucleotide"
BASE COUNT      10 a      11 c      9 g      3 t
ORIGIN
Query Match
Best Local Similarity 82.4%; Score 12.2; DB 6; Length 33;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGGAGGCAAGCTGGC 18
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    1 CCGGAGGCAAGCTGGC 18
Db 7 CCGGAGGCAAGCTGGC 23

RESULT 16
AX127337
LOCUS AX127337 50 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 57 from Patent EP1111055.
ACCESSION AX127337
VERSION AX127337.1 GI:14133508
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct.
        artificial sequences.
REFERENCE 1 (bases 1 to 50)
AUTHORS Strosberg,A.D. and Eshdat,Y.
TITLE Plant enzymes with phospholipid hydroperoxide glutathione
JOURNAL peroxidase activity, their analogues and their use
PATENT: EP 1111055-A 57 27-JUN-2001;
VELTIGEN (FR)
FEATURES
    source
        1. .50
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="primers"
BASE COUNT      11 a      10 c      12 g      17 t
ORIGIN
Query Match
Best Local Similarity 82.4%; Score 12.2; DB 6; Length 50;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY 1 CCCGAGGAGCTCTGG 17
||| ||||| |||||
Db 30 CCCACAGGAGCTCTGG 46

RESULT 17
AX384794/c AX384794 22 bp DNA linear PAT 19-MAR-2002
LOCUS Sequence 12 from Patent WO0191548.
DEFINITION AX384794
ACCESSION AX384794
VERSION AX384794.1 GI:19577929
KEYWORDS
SOURCE
ORGANISM
FEATURES
1
REFERENCE
1
AUTHORS
TITLE
JOURNAL
PHARMACIA & UPJOHN COMPANY (US)
Location/Qualifiers

FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 3 a 8 c 6 g 5 t
ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAGGAGCTCTGG 17
||||| ||||| |||||
Db 21 AAGGAGCTCTGG 10

RESULT 18
AR095087/c AR095087 23 bp DNA linear PAT 08-SEP-2000
LOCUS Sequence 2 from patent US 6002066.
DEFINITION AR095087
ACCESSION AR095087
VERSION AR095087.1 GI:10022625
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 23)
AUTHORS
TITLE
JOURNAL
H2-M modified transgenic mice
Patent: US 6002066-A 2 14-DEC-1999;
Location/Qualifiers

FEATURES
source
1..23
/organism="unknown"

BASE COUNT 5 a 8 c 5 g 5 t
ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAGGAGCTCTGG 17
||||| ||||| |||||
Db 23 AAGGAGCTCTGG 12

RESULT 19
AX447459/c AX447459 24 bp DNA linear PAT 03-JUL-2002
LOCUS Sequence 3914 from Patent WO0216649.
DEFINITION AX447459
ACCESSION AX447459
VERSION AX447459.1 GI:21696358

KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
Illumina, Inc. (US)
Location/Qualifiers

FEATURES
source
1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."

BASE COUNT 5 a 7 c 5 g 7 t
ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 CGGAGGAGCTC 14
||||| ||||| |||||
Db 19 CGGAGGAGCTC 8

RESULT 20
AR108592/c AR108592 26 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 1 from patent US 6110902.
DEFINITION AR108592
ACCESSION AR108592
VERSION AR108592.1 GI:12824079
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 26)
AUTHORS
TITLE
JOURNAL
Method for the inhibition of neuronal activity leading to a focal
epileptic seizure by local delivery of adenosine
Patent: US 6110902-A 1 29-AUG-2000;
Location/Qualifiers

FEATURES
source
1..26
/organism="unknown"

BASE COUNT 7 a 7 c 7 g 5 t
ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAGGAGCTCTGG 17
||||| ||||| |||||
Db 17 AAGGAGCTCTGG 6

RESULT 21
AX092972/c AX092972 26 bp DNA linear PAT 30-MAR-2001
LOCUS Sequence 31 from Patent WO0118225.
DEFINITION AX092972
ACCESSION AX092972
VERSION AX092972.1 GI:13509457
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 26)
AUTHORS
TITLE
JOURNAL
Targeting constructs and transgenic animals produced therewith
Patent: WO 0118225-A 31 15-MAR-2001;
Xenogen Corporation (US)
Location/Qualifiers

FEATURES
source
1..26

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/organism="synthetic construct"
/db_xref="taxon:32630"
/feature="primer R51"
BASE COUNT      6 a      9 c      7 g      4 t
ORIGIN

Query Match      66.7%; Score 12; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      6 AAGCAGCTCTGG 17
Db      12 AAGCAGCTCTGG 1

RESULT 22
BD012014/c      26 bp      DNA      linear      PAT 02-AUG-2002
LOCUS      Hydrocephalus model animal.
ACCESSION      BD012014
VERSION      BD012014.1 GI:22092203
KEYWORDS      MO 0101767-A/4.
SOURCE      synthetic construct.
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 26)
AUTHORS      Sakakibara,S., Noda,T. and Okano,H.
TITLE      Hydrocephalus model animal
JOURNAL      Patent: WO 0101767-A 4 11-JAN-2001;
              JAPAN SCIENCE AND TECHNOLOGY CORP,SHINICHI SAKAKIBARA,TETSUO NODA,
              HIDEYUKI OKANO
COMMENT      OS Artificial Sequence
              PN MO 0101767-A/4
              PD 11-JAN-2001
              PE 04-JUL-2000 MO 2000JP004449
              PR 05-JUL-1999 JP 99P 190796
              PI SHINICHI SAKAKIBARA,TETSUO NODA,HIDEYUKI OKANO PC
              AO1K67/027,A61K45/00,A61K49/00,A61K25/00,G01N33/50,G01N33/15 CC
              Artificial sequence: Synthesized oligonucleotide FH key
              Location/Qualifiers
              source      1..26
                          /organism="synthetic construct"
                          /db_xref="taxon:32630"
BASE COUNT      6 a      8 c      7 g      5 t
ORIGIN

Query Match      66.7%; Score 12; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      6 AAGCAGCTCTGG 17
Db      13 AAGCAGCTCTGG 2

RESULT 23
E55063/c      26 bp      DNA      linear      PAT 31-JAN-2002
LOCUS      Hydrocephalic model animal.
ACCESSION      E55063
VERSION      E55063.1 GI:18629732
KEYWORDS      JP 2001017027-A/4.
SOURCE      synthetic construct.
ORGANISM      synthetic construct.
REFERENCE      1 (bases 1 to 26)
AUTHORS      Sakakibara,S., Noda,T. and Okano,H.
TITLE      Hydrocephalic model animal
JOURNAL      Patent: JP 2001017027-A 4 23-JAN-2001;
              SCIENCE & TECH AGENCY
              OS Artificial Sequence
              PN JP 2001017027-A/4

/organism="synthetic construct"
/db_xref="taxon:32630"
/feature="primer R51"
BASE COUNT      6 a      9 c      7 g      4 t
ORIGIN

Query Match      66.7%; Score 12; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      6 AAGCAGCTCTGG 17
Db      13 AAGCAGCTCTGG 2

RESULT 24
BD004494/c      standard; DNA: SYN; 26 BP.
ID      BD004494
AC      BD004494;
XX      BD004494.1
SV      BD004494.1
DT      08-FEB-2002 (rel. 70. Created)
DI      08-FEB-2002 (rel. 70; last updated, Version 1)
XX      DE Hydrocephalus model animal.
XX      KM JP 03074376-T/4.
XX      OS synthetic construct
XX      OC artificial sequence.
XX      [1]
XX      RA Sakakibara S., Noda T., Okano H.;
XX      RT "Hydrocephalus model animal";
XX      RL Patent number JP03074376-T/4, 12-JAN-2001.
XX      JAPAN SCIENCE AND TECHNOLOGY CORP,SHINICHI SAKAKIBARA,TETSUO NODA, HIDEYUKI
XX      OKANO.
XX      OS Artificial Sequence
XX      PN JP 03074376-T/4
XX      CC PD 12-JUN-2001 JP 2000004449
XX      CC PF 04-JUL-2000 JP 2000004449
XX      CC PR 05-JUL-1999 JP 99P 190796
XX      CC PI SHINICHI SAKAKIBARA,TETSUO NODA,HIDEYUKI OKANO
XX      CC PC AO1K67/027,A61K45/00,A61K49/00,A61K25/00,G01N33/50,G01N33/15
XX      CC CC
XX      CC FH key
XX      CC FT source
XX      FT key      Location/Qualifiers
XX      FT source      1..26
                      /organism="Artificial Sequence"
XX      key      Location/Qualifiers
XX      source      1..26
                      /db_xref="taxon:32630"
                      /organism="synthetic construct"
XX      Sequence 26 BP: 6 A; 8 C; 7 G; 5 T; 0 other:
SQ

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Query Match 66.7%; Score 12; DB 23; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAGCAGTCTGG 17
|||||
DB 13 AAGCAGTCTGG 2

RESULT 25
BD012788/c
LOCUS BD012788 28 bp DNA linear PAT 02-AUG-2002
DEFINITION An animal with a knocked out alpha-tocopherol transfer protein gene.
ACCESSION BD012788
VERSION BD012788.1 GI:22092977
KEYWORDS WO 0113716-A/3.
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 28)
AUTHORS Inoue,K., Arai,H., Arita,M., Jishage,K. and Suzuki,H.
TITLE An animal with a knocked out alpha-tocopherol transfer protein gene
JOURNAL Patent: WO 0113716-A 3 01-MAR-2001;
KEIZO INOUE,HIROYUKI ARAI,MAKOTO ARITA,KOICHI JISHAGE, IROSHI SUZUKI
COMMENT OS Artificial Sequence
PN WO 0113716-A/3
PD 01-MAR-2001
PF 24-AUG-2000 WO 2000JP005686
PR 24-AUG-1999 JP 99P 237003
PI KEIZO INOUE,HIROYUKI ARAI,MAKOTO ARITA,KOICHI JISHAGE, PI HIROSHI SUZUKI
PC A01K67/027,C12N15/12,C12N5/06,C12N5/16,A61K45/00,A61P3/02, PC A61P9/10,
A61P3/10,G01N33/50,G01N33/15
CC
FH Key Location/Qualifiers.
FEATURES
source 1..28 Location/Qualifiers.
BASE COUNT 6 a 9 c 7 g 6 t
ORIGIN
Query Match 66.7%; Score 12; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAGCAGTCTGG 17
|||||
DB 27 AAGCAGTCTGG 16

RESULT 26
BD008223/c
ID BD008223 standard; DNA; SYN: 28 BP.
XX BD008223;
XX BD008223.1
SV
XX 08-FEB-2002 (Rel. 70, Created)
DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)
XX
DE An animal with a knocked out alpha-tocopherol transfer protein gene.
XX JP 03075485-T/3.
KW
XX synthetic construct
OC artificial sequence.
XX
RN [1]

RP 1-28
RA Inoue K., Arai H., Arita M., Jishage K., Suzuki H.;
RT "An animal with a knocked out alpha-tocopherol transfer protein gene";
RL Patent number JP03075485-T/3, 23-FEB-2001
RL KEIZO INOUE,HIROYUKI ARAI,MAKOTO ARITA,KOICHI JISHAGE, IROSHI SUZUKI.
XX
XX OS Artificial Sequence
CC PN JP 03075485-T/3
CC PD 23-FEB-2001
CC PF 24-AUG-2000 JP 2000005686
CC PR 24-AUG-1999 JP 99P 237003
CC PI KEIZO INOUE,HIROYUKI ARAI,MAKOTO ARITA,KOICHI JISHAGE,
CC PI HIROSHI SUZUKI
CC PC A01K67/027,C12N15/12,C12N5/06,C12N5/16,A61K45/00,A61P3/02,
CC PC A61P9/10,
CC PC A61P3/10,G01N33/50,G01N33/15
CC FH Key Location/Qualifiers
CC FT source 1..28
CC FT source Location/Qualifiers
FH Key Location/Qualifiers
FH source 1..28
FT /db_xref="taxon:32630"
FT /organism="synthetic construct"
XX
XX
SQ Sequence 28 BP; 6 A; 9 C; 7 G; 6 T; 0 other;

Query Match 66.7%; Score 12; DB 23; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAGCAGTCTGG 17
|||||
DB 27 AAGCAGTCTGG 16

RESULT 27
AX327013/c
LOCUS AX327013 20 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 209 from Patent WO0178894.
ACCESSION AX327013
VERSION AX327013.1 GI:18097724
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1
AUTHORS Keith,T.
TITLE Novel human gene relating to respiratory diseases, obesity, and inflammatory bowel disease
JOURNAL Patent: WO 0178894-A 209 25-OCT-2001;
Genome Therapeutics Corp. (US)
FEATURES
source 1..20 Location/Qualifiers
BASE COUNT 5 a 5 c 5 g 5 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 20;
Best Local Similarity 86.7%; Pred. No. 9.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCGGAGGCACTCT 15
|||||
DB 15 CCGGAGGCACTCT 1
RESULT 28
I32023/c

LOCUS 132023 21 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 34 from patent US 5585232.
ACCESSION 132023
VERSION 132023.1 GI:1822814
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Fair,S.B.
TITLE Methods and diagnostic kits for determining toxicity utilizing E.
JOURNAL coli stress promoters fused to reporter genes
FEATURES
source 1..21
location/Qualifiers
BASE COUNT 4 a 8 c 5 g 4 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 21;
Best Local Similarity 86.7%; Pred. No. 9e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CCGGAGGCGACTCT 15
Db 19 CCGGAGGCGGTTT 5
RESULT 29
LOCUS 132707 21 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 34 from patent US 5589337.
ACCESSION 132707
VERSION 132707.1 GI:1823498
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Fair,S.B.
TITLE Methods and diagnostic kits for determining toxicity utilizing
JOURNAL bacterial stress promoters fused to reporter genes
FEATURES
source 1..21
location/Qualifiers
BASE COUNT 4 a 8 c 5 g 4 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 21;
Best Local Similarity 86.7%; Pred. No. 9e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CCGGAGGCGACTCT 15
Db 19 CCGGAGGCGGTTT 5
RESULT 30
LOCUS AY082157 23 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 7 from Patent WO0109293.
ACCESSION AY082157
VERSION AY082157.1 GI:13170957
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Sheppard,P.O., Baidur,N. and Bishop,P.D.
TITLE Mamalian adhesion protease peptides
JOURNAL Patent: WO 0109293-A 7 08-FEB-2001;
zymogenetics, Inc. (US)

FEATURES
source Location/Qualifiers
1..23
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide ZC17,993"
BASE COUNT 5 a 6 c 6 g 6 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 23;
Best Local Similarity 86.7%; Pred. No. 8.8e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CCGGAGGCGACTCT 15
Db 7 CCGGAGGCGACTCT 21
RESULT 31
LOCUS AR198876 24 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 178 from patent US 6355411.
ACCESSION AR198876
VERSION AR198876.1 GI:20248950
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ausubel,F., Goodman,H.M., Rahne,L.G., Mahajan-Miklos,S., Tan,N.-W.,
TITLE Cao,H., Drenthard,E. and Tsongalis,J.
JOURNAL virulence-associated nucleic acid sequences and uses thereof
FEATURES
source 1..24
location/Qualifiers
BASE COUNT 5 a 7 c 9 g 3 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 8.7e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 CCGGAGGCGACTCTG 16
Db 9 CCGGAGGCGAGCTG 23
RESULT 32
LOCUS AX428028 25 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 5 from Patent WO0233105.
ACCESSION AX428028
VERSION AX428028.1 GI:21538077
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Creissen,G.P. and Mullineaux,P.M.
TITLE Methods and means for modification of plant characteristics
JOURNAL Patent: WO 0233105-A 5 25-APR-2002;
PLANT BIOSCIENCE LTD (GB)
FEATURES
source 1..25
location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"
BASE COUNT 4 a 5 c 9 g 7 t
ORIGIN
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Best Local Similarity 86.7%; Pred. No. 8.6e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCCGAGAGCACTCT 15
|||||
DB 8 CCCGAGAGCGGTTT 22

RESULT 33
A05131/c 45 bp DNA linear PAT 04-MAY-1993
LOCUS A05131
DEFINITION Oligonucleotide 19 for bovine growth hormone.

ACCESSION A05131
VERSION A05131.1 GI:345018
KEYWORDS

SOURCE synthetic construct.
ORGANISM synthetic construct
FEATURES artificial sequences.

FEATURES
source Location/Qualifiers
1..45
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 9 a 14 c 9 g 13 t
ORIGIN

Query Match 65.6%; Score 11.6; DB 6; Length 45;
Best Local Similarity 86.7%; Pred. No. 7.3e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAGGAGCTGGC 18
|||||
DB 20 GGAGGCACTCTGGC 6

RESULT 34
AX201806 22 bp DNA linear PAT 30-AUG-2001
LOCUS AX201806
DEFINITION Sequence 15 from Patent W00153537.
ACCESSION AX201806
VERSION AX201806.1 GI:15391652
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS I (bases 1 to 22)
TITLE Moskowitz,D.W.
JOURNAL Nitric oxide synthase gene diagnostic polymorphisms
Patent: WO 0153537-A 15 26-JUN-2001;

FEATURES
source Location/Qualifiers
1..22
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature 1..22
/note="STAR_1 (Se-Cys tRNA gene transcription activating factor)"
BASE COUNT 6 a 9 c 4 g 3 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 22;
Best Local Similarity 77.8%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGAGAGCACTCTGGC 18
|||||
DB 5 CCCAGATGCACTCTGGC 22

RESULT 35
E04526 25 bp DNA linear PAT 29-SEP-1997
LOCUS E04526
DEFINITION PCR primer.
ACCESSION E04526
VERSION E04526.1 GI:2172727

KEYWORDS JP 1993078397-A/1.
SOURCE synthetic construct.
ORGANISM synthetic construct
FEATURES artificial sequences.

REFERENCE 1 (bases 1 to 25)
AUTHORS Yamazaki,C., Takasu,N., Negoro,T. and Agui,H.
TITLE THROMBOLYTIC PROTEIN
JOURNAL Patent: JP 1993078397-A 1 30-MAR-1993;
SUMITOMO PHARMACEUT CO LTD

COMMENT OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1993078397-A/1
PD 30-MAR-1993

PI YAMAZAKI CHIE, TAKASU NOKO, NEGORO TAKASU, AGUI HIDEO PC
C07K13/00,A61K37/24,A61K37/54,C12N1/19,C12N1/21,C12N5/10, PC
C12N9/64,
PC C12N15/58,C12N15/62,C12N15/70,C12N15/81,C12N15/85//C12P21/02,
PC (C12N1/21,
PC C12R1:19),(C12P21/02,C12R1:19);
CC strandedness: Single;
CC topology: linear.

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 3 a 10 c 9 g 3 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 25;
Best Local Similarity 77.8%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGAGAGCACTCTGGC 18
|||||
DB 2 CCTGAGAGGAGCGGC 19

RESULT 36
AR143851 27 bp DNA linear PAT 08-AUG-2001
LOCUS AR143851
DEFINITION Sequence 113 from patent US 6205404.
ACCESSION AR143851
VERSION AR143851.1 GI:15105137
KEYWORDS

SOURCE unknown.
ORGANISM unknown.

REFERENCE Unclassified.
1 (bases 1 to 27)
AUTHORS Michaels,G.S., Mikelisaar,R.-H. and Feldmann,R.J.
TITLE DNA-binding proteins of the zinc-finger class
JOURNAL Patent: US 6205404-A 113 20-MAR-2001;

FEATURES
source Location/Qualifiers
1..27
/organism="unknown"
BASE COUNT 8 a 7 c 10 g 2 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 27;
Best Local Similarity 77.8%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGAGAGCACTCTGGC 18
|||||
DB 1 CCAGGAGGCGCACTGGC 18

RESULT 37
AX248747 31 bp DNA linear PAT 28-SEP-2001
LOCUS AX248747
DEFINITION Sequence 826 from Patent W00166800.
ACCESSION AX248747
VERSION AX248747.1 GI:15863370

KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 31)
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 826 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
Source Location/Qualifiers
1..31
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 4 a 9 c 13 g 4 t 1 others
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 31;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGTGCC 18
Db 12 CCTTAAAGCGCGCTGTGCC 29

RESULT 38
AX399412 33 bp DNA linear PAT 28-MAY-2002
LOCUS AX399412
DEFINITION Sequence 16 from Patent WO204680.
ACCESSION AX399412
VERSION AX399412.1 GI:21261983
KEYWORDS
ORGANISM Thermus aquaticus.
SOURCE Thermus aquaticus
REFERENCE 1
AUTHORS Hardin,S.H., Briggs,J.M., Tu,S.C., Gao,X. and Willson,R.
TITLE Real-time sequence determination
JOURNAL Patent: WO 0204680-A 16 17-JAN-2002;
VISIGEN Biotechnologies, Inc. (US)
FEATURES
Source Location/Qualifiers
1..33
/organism="Thermus aquaticus"
/db_xref="taxon:271"

variation
16..18
/note="Tag Pol I Mutation: AA 655 asp to cys: codon: gac
-> tgc"

BASE COUNT 2 a 14 c 13 g 4 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 33;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGTGCC 18
Db 2 CCCGGAGGCGCGTGTGCC 19

RESULT 39
AX399413 33 bp DNA linear PAT 28-MAY-2002
LOCUS AX399413
DEFINITION Sequence 17 from Patent WO204680.
ACCESSION AX399413
VERSION AX399413.1 GI:21261984
KEYWORDS
ORGANISM Thermus aquaticus.
SOURCE Thermus aquaticus
REFERENCE 1
Thermaceae; Thermus.

AUTHORS Hardin,S.H., Briggs,J.M., Tu,S.C., Gao,X. and Willson,R.
TITLE Real-time sequence determination
JOURNAL Patent: WO 0204680-A 17 17-JAN-2002;
VISIGEN Biotechnologies, Inc. (US)
FEATURES
Source Location/Qualifiers
1..33
/organism="Thermus aquaticus"
/db_xref="taxon:271"

variation
16..18
/note="Tag Pol I Mutation Complimentary Strand: AA 516
655 asp to cys: antisense codon: gtc -> gca. 5' to 3'
listing."

BASE COUNT 4 a 13 c 14 g 2 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 33;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGTGCC 18
Db 32 CCCGGAGGCGCGTGTGCC 15

RESULT 40
AX297519 44 bp DNA linear PAT 21-NOV-2001
LOCUS AX297519
DEFINITION Sequence 9281 from Patent WO0179548.
ACCESSION AX297519
VERSION AX297519.1 GI:17059210
KEYWORDS
ORGANISM synthetic construct.
SOURCE synthetic construct
REFERENCE 1
AUTHORS Barany,F., Zivri,M., Gerry,N.P., Favis,R. and Kilman,R.
TITLE Method of designing an addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
PATENT: WO 0179548-A 9281 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
Source Location/Qualifiers
1..44
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Consensus Primer Sequence"

BASE COUNT 11 a 11 c 15 g 7 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 44;
Best Local Similarity 77.8%; Pred. No. 9.2e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGTGCC 18
Db 20 CCCGTAAAGCCGCTATGTGCC 37

Search completed: December 2, 2002, 13:33:44
Job time : 2679 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 12:36:58 : Search time 252 Seconds

(without alignments)
160.857 Million cell updates/sec

Title: US-09-848-868-35

Sequence: 1 ccgcgaagcagctctgac 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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21: /SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	24	AA519106 Human p53 coding s
2	18	100.0	36	24	AA519107 Human p53 coding s
3	18	100.0	37	20	AA265511 WO 9909191 Segid #
4	15	83.3	25	15	AA061823 Primer for mutant
5	14.8	82.2	26	22	AA068956 PCR primer used to
6	13.2	73.3	21	24	AA142029 T. reesei endogluc
7	13.2	73.3	27	24	AA142028 T. reesei endogluc
8	12.8	71.1	18	17	AA150605 Human CERP hairpin
9	12.8	71.1	18	17	AA150701 Rabbit CERP hairpin

C	10	12.8	71.1	28	16	AA092447	CD3 delta chain 3'
C	11	12.8	71.1	30	11	AA006064	N-terminus probe u
C	12	12.4	68.9	18	17	AA150604	Human CERP hairpin
C	13	12.4	68.9	18	17	AA150700	Rabbit CERP hairpin
C	14	12.4	68.9	26	21	AA087923	Human beta-3-adren
C	15	12.2	67.8	17	24	ABK33460	Human TNF-receptor
C	16	12.2	67.8	20	14	AA050876	HSV2 primer. Synt
C	17	12.2	67.8	20	14	AA050876	PCR primer. Synt
C	18	12.2	67.8	20	24	AA155599	PCR primer #5 used
C	19	12.2	67.8	20	24	AB022225	Human/calmodulin 1
C	20	12.2	67.8	26	20	AA089117	PCR primer for HIV
C	21	12.2	67.8	32	16	AA087560	HTLVIII amplifica
C	22	12.2	67.8	32	16	AA089758	Primer XHOM to amp
C	23	12.2	67.8	33	20	AA211413	Oligo for mutating
C	24	12.2	67.8	36	21	AA074925	Nucleotide sequenc
C	25	12.2	67.8	46	21	AA074926	Nucleotide sequenc
C	26	12.2	67.8	50	22	AA127830	Nucleotide sequenc
C	27	12.2	67.8	50	22	AA127830	Human SNP oligonuc
C	28	12.2	67.8	50	22	AA127830	pig PGPx 3' UTR o
C	29	12.2	67.8	50	22	AA127830	Wolfram Syndrome 1
C	30	12.2	67.8	23	19	AA041645	Nucleotide sequenc
C	31	12.2	67.8	24	24	AA033907	ADA knock-out spec
C	32	12.2	67.8	26	20	AA009363	PKR-LR-VN/VEGF 5' tr
C	33	12.2	67.8	26	22	AA010772	Mouse Musashi 1 PC
C	34	12.2	67.8	28	22	AA062210	PCR primer for PKG
C	35	12.2	67.8	28	24	AB070370	Human Neurogenin-3
C	36	12.2	67.8	28	24	AA065981	Human map-related
C	37	12.2	67.8	47	21	AA065981	Human IL-4 receptor
C	38	11.8	65.6	15	18	AA076214	Human IL-4 receptor
C	39	11.8	65.6	15	21	AA054609	Human IL4 receptor
C	40	11.8	65.6	15	21	AA054609	Human IL4 receptor
C	41	11.8	65.6	15	21	AA033453	Low adenosine anti I
C	42	11.8	65.6	15	22	AA049083	IGF-I oligonucleot
C	43	11.8	65.6	15	22	AA052897	IGF-I oligonucleot
C	44	11.8	65.6	17	24	ABN01478	Human GDMPLP-1 17-m
C	45	11.8	65.6	17	24	ABN01478	Human GDMPLP-1 17-m
C	46	11.8	65.6	20	21	AA082974	Human IGF-1 antisec
C	47	11.8	65.6	20	21	AA082974	Human IGF-1 antisec
C	48	11.8	65.6	20	21	AA045382	gsh-lacZ fusion co
C	49	11.8	65.6	21	15	AA054942	Reverse primer R3
C	50	11.8	65.6	21	20	AA074050	Enzymatic DNA RNA
C	51	11.8	65.6	21	20	AA074050	Primer used to amp
C	52	11.8	65.6	23	22	AA085519	Glutathione synthet
C	53	11.8	65.6	24	20	AA098260	Human GDMPLP-1 25-m
C	54	11.8	65.6	25	24	ABN04407	Human GDMPLP-1 25-m
C	55	11.8	65.6	25	24	ABN04407	Human GDMPLP-1 25-m
C	56	11.8	65.6	25	24	ABN04408	Human GDMPLP-1 25-m
C	57	11.8	65.6	25	24	ABN04409	Human GDMPLP-1 25-m
C	58	11.8	65.6	25	24	ABN04410	Human GDMPLP-1 25-m
C	59	11.8	65.6	25	24	ABN04411	Human GDMPLP-1 25-m
C	60	11.8	65.6	25	24	ABN04412	Human GDMPLP-1 25-m
C	61	11.8	65.6	25	24	ABN04413	Human GDMPLP-1 25-m
C	62	11.8	65.6	25	24	ABN04414	Human GDMPLP-1 25-m
C	63	11.8	65.6	25	24	ABN04415	Human GDMPLP-1 25-m
C	64	11.8	65.6	25	24	ABN04416	Human GDMPLP-1 25-m
C	65	11.8	65.6	25	24	ABN04417	Human GDMPLP-1 25-m
C	66	11.8	65.6	33	22	AA062818	Dpnt endonuclease
C	67	11.8	65.6	40	18	AA048227	Human RelA(p65) mr
C	68	11.8	65.6	41	21	AA015263	PCR primer used fo
C	69	11.8	65.6	41	21	AA015264	PCR primer for a m
C	70	11.8	65.6	47	21	AA068926	Human map-related
C	71	11.8	65.6	49	21	AA015278	PCR primer for a m
C	72	11.8	65.6	50	17	AA029107	Human SNP oligonuc
C	73	11.8	65.6	50	17	AA029107	Primer used in rec
C	74	11.6	64.4	22	12	AA023166	Nitric oxide synth
C	75	11.6	64.4	25	14	AA041194	PCR primer to ampl
C	76	11.6	64.4	27	20	AA027139	Caenorhabditis ele
C	77	11.6	64.4	29	18	AA020189	Human foetal liver
C	78	11.6	64.4	29	21	AA092450	Type C lectin PCR
C	79	11.6	64.4	31	22	ABK30338	Human single nucle
C	80	11.6	64.4	33	24	ABK40144	DNA polymerase I f
C	81	11.6	64.4	33	24	ABK40145	Coagulation factor
C	82	11.6	64.4	40	24	ABN88587	

83	11.6	64.4	44	24	AB182087	K-ras mutation det	c 156	11.2	62.2	26	20	AAV72127
c 84	11.6	64.4	45	22	AA564186	Human prostate cdn	c 157	11.2	62.2	27	17	AA11697
c 85	11.6	64.4	48	20	AA210910	Probe #2 for adeny	c 158	11.2	62.2	27	23	AAH78704
c 86	11.6	64.4	50	22	AA129297	Human SNP oligonuc	c 159	11.2	62.2	27	24	AA517030
c 87	11.6	64.4	50	22	AA123396	Human SNP oligonuc	c 160	11.2	62.2	27	24	AA067014
c 88	11.6	64.4	50	22	AA132397	Human SNP oligonuc	c 161	11.2	62.2	28	15	AAV82714
c 89	11.6	64.4	50	22	AA134260	Human SNP oligonuc	c 162	11.2	62.2	28	21	AAAV6314
c 90	11.6	64.4	50	22	AA134540	Human SNP oligonuc	c 163	11.2	62.2	28	21	AAAB9549
c 91	11.6	64.4	50	22	AA175365	Human silent SNP c	c 164	11.2	62.2	28	22	AA502157
c 92	11.4	63.3	20	24	AA143513	Human DB2 antisen	c 165	11.2	62.2	28	22	AA502175
c 93	11.4	63.3	21	17	AA133465	MKP gene antisense	c 166	11.2	62.2	28	22	AAE82040
c 94	11.4	63.3	21	22	AAE95866	Human gene single	c 167	11.2	62.2	28	22	AAE84690
c 95	11.4	63.3	21	22	AAE95861	Human MRP antisens	c 168	11.2	62.2	28	22	AAE77865
c 96	11.4	63.3	22	22	AAE92242	Human IGBR coding	c 169	11.2	62.2	28	22	AAE79726
c 97	11.4	63.3	24	24	AB161087	RNA uncoding enzy	c 170	11.2	62.2	28	22	AAE81158
c 98	11.4	63.3	25	22	AAAO7400	PCR primer for C5L	c 171	11.2	62.2	28	22	AAE75779
c 99	11.4	63.3	25	22	AAH38135	SNP specific SNPE	c 172	11.2	62.2	28	22	AAE77556
c 100	11.4	63.3	26	22	AA504013	Rhesus gene locus:	c 173	11.2	62.2	28	22	AAE59738
c 101	11.4	63.3	28	22	AAAD20452	P. syringae pv. to	c 174	11.2	62.2	29	17	AAAT33579
c 102	11.4	63.3	29	24	ABK96413	PCR primer OGR25 f	c 175	11.2	62.2	29	17	AAAT9638
c 103	11.4	63.3	36	24	ABA97262	Mutagenic primer 1	c 176	11.2	62.2	29	20	AAV64110
c 104	11.4	63.3	36	16	AA704582	Mutagenic primer 2	c 177	11.2	62.2	30	12	AAO13244
c 105	11.4	63.3	38	22	AAE69818	Sense primer for h	c 178	11.2	62.2	30	21	AA231659
c 106	11.4	63.3	39	22	AAE69818	Human IL4Ralpha ge	c 179	11.2	62.2	32	21	AAV22413
c 107	11.4	63.3	39	22	AAE69823	Human IL4Ralpha ge	c 180	11.2	62.2	32	24	AA168048
c 108	11.4	63.3	39	22	AAE69836	Human IL4Ralpha ge	c 181	11.2	62.2	34	20	AAZ00715
c 109	11.4	63.3	39	22	AAE69847	Human IL4Ralpha ge	c 182	11.2	62.2	34	21	AAAV1912
c 110	11.4	63.3	47	21	AAZ68989	Human map-related	c 183	11.2	62.2	35	20	AAAV16949
c 111	11.4	63.3	49	18	AA780464	Hepatoma AS-30D Ty	c 184	11.2	62.2	35	21	AAZ91587
c 112	11.2	62.2	17	24	AAAD23904	Human transferrin	c 185	11.2	62.2	36	24	ABA97265
c 113	11.2	62.2	18	21	AAZ36581	Probe hybridizing	c 186	11.2	62.2	36	24	ABA97266
c 114	11.2	62.2	18	24	AB143392	Human chromosome 1	c 187	11.2	62.2	37	14	AAO49129
c 115	11.2	62.2	20	15	AAO55806	anol gene primer.	c 188	11.2	62.2	38	22	AAAH9077
c 116	11.2	62.2	20	20	AAO90955	Tumour necrosis fa	c 189	11.2	62.2	41	19	AAV37843
c 117	11.2	62.2	20	22	AAH76243	Human macrophage-d	c 190	11.2	62.2	41	20	AAK56674
c 118	11.2	62.2	20	22	AAH81191	Human bcl-6 phosph	c 191	11.2	62.2	42	13	AAO21357
c 119	11.2	62.2	20	24	ABK51698	Human CRH receptor	c 192	11.2	62.2	42	18	AAV02266
c 120	11.2	62.2	21	21	AAH88066	Human zcaci-1 PCR	c 193	11.2	62.2	42	18	AAH66099
c 121	11.2	62.2	21	21	AAZ60648	PCR primer used to	c 194	11.2	62.2	44	24	AB182083
c 122	11.2	62.2	21	22	AAH60652	PCR primer used to	c 195	11.2	62.2	45	8	AAH70499
c 123	11.2	62.2	21	22	AAH85762	Proclactin reverse	c 196	11.2	62.2	46	22	AAE85184
c 124	11.2	62.2	21	24	ABF97639	Human gene single	c 197	11.2	62.2	46	22	AAE85186
c 125	11.2	62.2	21	24	ABK65421	Human single nucle	c 198	11.2	62.2	47	21	AAZ68421
c 126	11.2	62.2	22	18	AAH63390	Primer for C-termi	c 199	11.2	62.2	47	21	AAZ68456
c 127	11.2	62.2	22	21	AAO44744	Human DAXX gene ex	c 200	11.2	62.2	48	15	AAO62437
c 128	11.2	62.2	23	21	AAAC67954	Rat Erba receptor	c 201	11.2	62.2	50	22	AA129784
c 129	11.2	62.2	24	15	AAO77751	Beta-actin PCR pri	c 202	11.2	62.2	50	22	AA130994
c 130	11.2	62.2	24	21	AAAC63899	Chinese hamster be	c 203	11.2	62.2	50	22	AA176591
c 131	11.2	62.2	24	21	AAAC63901	Rat beta-actin RT-	c 204	11.2	61.1	15	24	AB188317
c 132	11.2	62.2	24	21	AAAG93888	Reverse PCR primer	c 205	11.2	61.1	17	18	AAH75252
c 133	11.2	62.2	24	21	AAAI2788	PCR primer ace2e8c	c 206	11.2	61.1	18	18	AAH75648
c 134	11.2	62.2	24	22	AA171185	Human beta actin p	c 207	11.2	61.1	20	22	AAH73035
c 135	11.2	62.2	24	22	AA507960	Human G-protein co	c 208	11.2	61.1	27	13	AAO22942
c 136	11.2	62.2	24	22	AA508276	Human G-protein co	c 209	11.2	61.1	27	14	AAO48200
c 137	11.2	62.2	24	22	AAE82281	Human beta CDNA PC	c 210	11.2	61.1	27	14	AAH78840
c 138	11.2	62.2	24	22	AAE30649	Human HDGFX hyprid	c 211	11.2	61.1	27	22	AAH75341
c 139	11.2	62.2	24	22	AAE30652	Human HDGFX hyprid	c 212	11.2	61.1	29	20	AAV92263
c 140	11.2	62.2	24	24	ABN88996	Human beta-actin p	c 213	11.2	61.1	31	21	AAAV9070
c 141	11.2	62.2	24	24	ABK50042	Beta actin reverse	c 214	11.2	61.1	38	10	AAAG4509
c 142	11.2	62.2	24	24	ABK50044	Rat beta actin rev	c 215	11.2	61.1	38	10	AAE69788
c 143	11.2	62.2	24	24	ABK70046	Antibody productio	c 216	11.2	61.1	39	22	AAE69795
c 144	11.2	62.2	24	24	ABK70048	NHF4-alpha protein	c 217	11.2	61.1	42	15	AAO69251
c 145	11.2	62.2	24	24	ABK47946	Beta 1,3-N-acetylgl	c 218	11.2	61.1	42	15	AAAT63713
c 146	11.2	62.2	24	24	ABL50788	ace2e8c PCR primer	c 219	11.2	61.1	42	20	AAAX17001
c 147	11.2	62.2	24	24	AAAD32610	Oligonucleotide ad	c 220	11.2	61.1	42	24	ABK82482
c 148	11.2	62.2	25	24	ABO03457	Human Klu6 PCR pri	c 221	10.8	60.0	15	22	AAE69569
c 149	11.2	62.2	25	22	AAE31891	Fungal probe SEQ ID	c 222	10.8	60.0	15	22	AAE49082
c 150	11.2	62.2	25	24	ABN99557	Fungal probe SEQ ID	c 223	10.8	60.0	15	22	AAE49084
c 151	11.2	62.2	25	24	ABN99575	Penicillium citrin	c 224	10.8	60.0	15	22	AAE52896
c 152	11.2	62.2	25	24	ABK29154	Penicillium janthi	c 225	10.8	60.0	15	22	AAE52898
c 153	11.2	62.2	25	24	ABK29172	Human catalytic te	c 226	10.8	60.0	16	15	AAO56019
c 154	11.2	62.2	26	20	AAV72136		c 227	10.8	60.0	16	15	AAO56020
c 155	11.2	62.2	26	20	AAV72140		c 228	10.8	60.0	16	15	AAO56022

Human catalytic te
5' primer for yeas
Human procollagen
Yeast cyclohexamid
Endoglucanase type
Partial sequence o
Xyloglucan endoglu
Xyloglucan endoglu
Partial DNA #7 enc
Partial DNA #7 enc
Xyloglucan endoglu
Partial nucleotide
Partial XGU endogl
Aspergillus aculea
Aspergillus aculea
Partial XGU endogl
A. aculeatus Xylogl
A. aculeatus CBS 1
PCR primer MB108 u
Primer MB108 for m
HSV-2 gH gene PCR
Splint probe C4bp.
PCR primer for hum
Human telomerase r
Epithelone PKS gen
Human telomerase c
Human telomerase c
Primer #12 for con
M13X11 construct
Mutagenic primer 1
Mutagenic primer 2
A. pleuropneumonia
CD4 human T-Lymph
Primer 47. Synthe
IL-6R CDR primer p
Human parathyroid
Human parathyroid
K-ras mutation det
Consensus repeat s
PCR primer for DNA
PCR primer for DNA
Human map-related
Human map-related
Vector pVAC1 const
Human SNP oligonuc
Human SNP oligonuc
Human silent SNP c
Human CHRE allele
Mouse flt-1 VEGF r
Mouse flt-1 VEGF r
Human dexx inhibit
Sequence of primer
PCR primer for amp
MusK1380F primer u
PCR primer used to
Human A-Raf hamme
Human genomic DNA
Probe for N-termi
Human IL4Ralpha po
Human IL4Ralpha po
Human ferredoxin g
Human ferredoxin g
Test sequence from
DNA binding molecu
Human IL4Ralpha ge
IGF-1 oligonucleot
IGF-1 oligonucleot
IGF-1 oligonucleot
IGF-1 oligonucleot
Bifidobacterium an
Bifidobacterium br
Bifidobacterium in

229	10.8	60.0	16	15	AA056023	Blifidbacterium lo	c 302	10.8	60.0	31	22	AA130846	Human single nucle
230	10.8	60.0	16	24	ABU51557	Human replication	c 303	10.8	60.0	31	22	AA131266	Human single nucle
231	10.8	60.0	16	24	ABK29399	Penicillium olsoni	c 304	10.8	60.0	31	24	ABK52374	Glucose dehydrogen
232	10.8	60.0	17	18	AAx73280	Mouse Elk-1 VEGF r	c 305	10.8	60.0	31	24	ABK21197	Human ERG DNazyme,
233	10.8	60.0	17	18	AAx73279	Mouse Elk-1 VEGF r	c 306	10.8	60.0	32	15	AAQ38728	Primer OMB19, Syn
234	10.8	60.0	17	24	ABN01477	Human GDM-LP-1 17-m	c 307	10.8	60.0	32	15	AAQ78763	Human alpha-galact
235	10.8	60.0	17	24	ABN01481	Human GDM-LP-1 17-m	c 308	10.8	60.0	32	15	AAQ66244	Alpha-galactosidas
236	10.8	60.0	17	24	ABN02219	Human GDM-LP-1 17-m	c 309	10.8	60.0	34	17	AAQ59161	Primer for amplify
237	10.8	60.0	17	24	ABN02220	Human GDM-LP-1 17-m	c 310	10.8	60.0	34	17	AAAT7206	SRE-2BP DNA bindin
238	10.8	60.0	17	24	ABN02221	Human GDM-LP-1 17-m	c 311	10.8	60.0	37	22	AAV18765	Primer LF394 for C
239	10.8	60.0	17	24	ABN02222	Human GDM-LP-1 17-m	c 312	10.8	60.0	40	20	AAH70278	Human cervical can
240	10.8	60.0	17	24	ABK17963	Human ERG hamsterhe	c 313	10.8	60.0	40	20	AAI19800	Drosophila antenna
241	10.8	60.0	17	24	ABK18758	Human ERG DNazyme	c 314	10.8	60.0	40	21	AAZ07766	P. melanogaster PA
242	10.8	60.0	17	24	ABL30538	Human HLA genocyp1	c 315	10.8	60.0	41	15	AAQ68309	PCR primer 9BP.6Q
243	10.8	60.0	18	7	AAAN60539	Sequence of probe	c 316	10.8	60.0	41	15	AAQ68309	Diabody primer LIN
244	10.8	60.0	18	20	AAZ01332	PCR primer for Pgl	c 317	10.8	60.0	41	15	AAQ56673	Primer 46, Synthe
245	10.8	60.0	19	21	AAAZ2682	PCR primer for amp	c 318	10.8	60.0	42	13	AAQ23843	Primer RHuVlamdbd
246	10.8	60.0	19	21	AAAZ3827	Human fetal brain	c 319	10.8	60.0	42	13	AAQ23844	Primer RHuVlamdbd
247	10.8	60.0	19	23	AAAT3749	Simple sequence re	c 320	10.8	60.0	42	13	AAQ23848	Primer RHuVlamdbd
248	10.8	60.0	20	17	AAAT13325	IGF 1R ATP-directe	c 321	10.8	60.0	42	24	AAQ28857	Human antibody cha
249	10.8	60.0	20	17	AAAT13326	IGF 1R ATP-directe	c 322	10.8	60.0	42	24	AAQ28858	Human antibody cha
250	10.8	60.0	20	19	AAV57182	Human Notch-3 muta	c 323	10.8	60.0	42	24	AAQ28858	p53 mutation detec
251	10.8	60.0	20	19	AAV57101	Human Notch3 mutat	c 324	10.8	60.0	43	24	AAQ28857	Human antibody cha
252	10.8	60.0	20	20	AAAT11998	Human potassium ch	c 325	10.8	60.0	47	20	AAQ21092	Probe for human PC
253	10.8	60.0	20	20	AAAZ7171	F primer for human GM	c 326	10.8	60.0	47	21	AAAZ01169	PCR primer for det
254	10.8	60.0	20	21	AAAZ7384	Probe for human GM	c 327	10.8	60.0	47	21	AAAZ7656	VEGF 2'-NH2-RNA nu
255	10.8	60.0	20	24	ABN85571	Human beta actin p	c 328	10.8	60.0	48	15	AAQ62436	Human SNP oligonuc
256	10.8	60.0	20	24	ABK69390	Chimeric phosphoro	c 329	10.8	60.0	50	16	AAQ88983	Human silent SNP c
257	10.8	60.0	20	24	ABAO2226	Human/mouse C/EBP	c 330	10.8	60.0	50	22	AAI74239	Human transcriptio
258	10.8	60.0	21	17	ABAI16424	Primer #1 for SWSS	c 331	10.8	60.0	50	22	AAI75329	Human silent SNP c
259	10.8	60.0	21	20	AAZ28423	Plus strand PCR pr	c 332	10.8	60.0	50	22	AAI75329	Human transcriptio
260	10.8	60.0	21	20	AAAZ9022	Human transcriptio	c 333	10.8	60.0	50	22	AAI75329	Human transcriptio
261	10.8	60.0	21	21	AAAC62619	Human OB gene sequ	c 334	10.8	60.0	50	22	AAAZ95074	Human osterilin ex
262	10.8	60.0	21	21	AAAC62619	Human OB gene sequ	c 335	10.8	60.0	50	22	AAAZ95074	Human osterilin ex
263	10.8	60.0	21	21	AAAT2341	Human OB DNA PCR p	c 336	10.8	60.0	50	22	AAI75329	Human osterilin ex
264	10.8	60.0	22	17	AAAT33366	Poly(ADP-ribose) P	c 337	10.8	60.0	50	22	AAI75329	Human osterilin ex
265	10.8	60.0	22	22	AAV65148	Ehrlichia sp. E80	c 338	10.8	60.0	50	22	AAI75329	Human osterilin ex
266	10.8	60.0	22	22	AAV65148	Human CPTFR real-tl	c 339	10.8	60.0	50	22	AAI75329	Human osterilin ex
267	10.8	60.0	22	22	AAV65148	Tall primer #14 fir	c 340	10.8	60.0	50	22	AAI75329	Human osterilin ex
268	10.8	60.0	23	23	ABAO1990	Pregnancy associat	c 341	10.8	60.0	50	22	AAI75329	Human osterilin ex
269	10.8	60.0	23	24	ABK22644	Human ERG Genebioc	c 342	10.8	60.0	50	22	AAI75329	Human osterilin ex
270	10.8	60.0	23	24	ABK22644	Human ERG Genebioc	c 343	10.8	60.0	50	22	AAI75329	Human osterilin ex
271	10.8	60.0	24	22	AAAF55566	PCR primer used to	c 344	10.8	60.0	50	22	AAI75329	Human osterilin ex
272	10.8	60.0	24	22	ABN04406	Human GDM-LP-1 25-m	c 345	10.8	60.0	50	22	AAI75329	Human osterilin ex
273	10.8	60.0	25	24	ABN04418	Human GDM-LP-1 25-m	c 346	10.8	60.0	50	22	AAI75329	Human osterilin ex
274	10.8	60.0	25	24	ABN05148	Human GDM-LP-1 25-m	c 347	10.8	60.0	50	22	AAI75329	Human osterilin ex
275	10.8	60.0	25	24	ABN05149	Human GDM-LP-1 25-m	c 348	10.8	60.0	50	22	AAI75329	Human osterilin ex
276	10.8	60.0	25	24	ABN05150	Human GDM-LP-1 25-m	c 349	10.8	60.0	50	22	AAI75329	Human osterilin ex
277	10.8	60.0	25	24	ABN05151	Human GDM-LP-1 25-m	c 350	10.8	60.0	50	22	AAI75329	Human osterilin ex
278	10.8	60.0	25	24	ABN05152	Human GDM-LP-1 25-m	c 351	10.8	60.0	50	22	AAI75329	Human osterilin ex
279	10.8	60.0	25	24	ABN05153	Human GDM-LP-1 25-m	c 352	10.8	60.0	50	22	AAI75329	Human osterilin ex
280	10.8	60.0	25	24	ABN05154	Human GDM-LP-1 25-m	c 353	10.8	60.0	50	22	AAI75329	Human osterilin ex
281	10.8	60.0	25	24	ABN05155	Human GDM-LP-1 25-m	c 354	10.8	60.0	50	22	AAI75329	Human osterilin ex
282	10.8	60.0	25	24	ABN05156	Human GDM-LP-1 25-m	c 355	10.8	60.0	50	22	AAI75329	Human osterilin ex
283	10.8	60.0	25	24	ABN05157	Human GDM-LP-1 25-m	c 356	10.8	60.0	50	22	AAI75329	Human osterilin ex
284	10.8	60.0	25	24	ABN05158	Human GDM-LP-1 25-m	c 357	10.8	60.0	50	22	AAI75329	Human osterilin ex
285	10.8	60.0	25	24	ABN05159	Human GDM-LP-1 25-m	c 358	10.8	60.0	50	22	AAI75329	Human osterilin ex
286	10.8	60.0	26	18	AAE61857	Human GDM-LP-1 25-m	c 359	10.8	60.0	50	22	AAI75329	Human osterilin ex
287	10.8	60.0	26	22	AAE28790	Hairpin nucleic ac	c 360	10.8	60.0	50	22	AAI75329	Human osterilin ex
288	10.8	60.0	26	22	AAE28791	Human GABA(b) rece	c 361	10.8	60.0	50	22	AAI75329	Human osterilin ex
289	10.8	60.0	26	22	AAE17071	Information carryl	c 362	10.8	60.0	50	22	AAI75329	Human osterilin ex
290	10.8	60.0	26	22	AAE19291	G protein-coupled	c 363	10.8	60.0	50	22	AAI75329	Human osterilin ex
291	10.8	60.0	28	24	ABK66752	Human gene specifl	c 364	10.8	60.0	50	22	AAI75329	Human osterilin ex
292	10.8	60.0	29	20	AAAZ83531	Primer A3 P2491/Q2	c 365	10.8	60.0	50	22	AAI75329	Human osterilin ex
293	10.8	60.0	29	20	AAAZ83535	Primer Lowa3 for m	c 366	10.8	60.0	50	22	AAI75329	Human osterilin ex
294	10.8	60.0	29	21	AAAZ9101	Human Rab24 PCR pr	c 367	10.8	60.0	50	22	AAI75329	Human osterilin ex
295	10.8	60.0	29	21	AAAZ9103	Human Rab24 PCR pr	c 368	10.8	60.0	50	22	AAI75329	Human osterilin ex
296	10.8	60.0	29	21	AAAZ9103	Human Rab24 PCR pr	c 369	10.8	60.0	50	22	AAI75329	Human osterilin ex
297	10.8	60.0	29	24	ABN81596	Escherichia coli w	c 370	10.8	60.0	50	22	AAI75329	Human osterilin ex
298	10.8	60.0	30	20	AAZ30466	Human FGF23 protei	c 371	10.8	60.0	50	22	AAI75329	Human osterilin ex
299	10.8	60.0	30	20	AAAZ6174	Primer 19 for toba	c 372	10.8	60.0	50	22	AAI75329	Human osterilin ex
300	10.8	60.0	30	22	AAI94449	Human Slt1-1 PCR p	c 373	10.8	60.0	50	22	AAI75329	Human osterilin ex
301	10.8	60.0	31	22	AAI29594	Human hdbd-1 contr	c 374	10.8	60.0	50	22	AAI75329	Human osterilin ex
						Human single nucle							

C 375	10.6	58.9	21	17	AAAT10459	Anti-HIV TAR regio	C 448	10.6	58.9	38	21	AAZ55102	Neisseria species
C 376	10.6	58.9	21	18	AAAT92446	TAT system oligonu	C 449	10.6	58.9	38	22	AAAF31703	Human NF-AT polyu
C 377	10.6	58.9	21	19	AAAT64326	Antisense oligonuc	C 450	10.6	58.9	38	24	AAD34029	Human NF-AT polyu
C 378	10.6	58.9	21	19	AAV48412	Transforming growt	C 451	10.6	58.9	39	22	AAAF69796	Human IL4Ra1pha po
C 379	10.6	58.9	21	19	AAV38643	Human ICAM-1, E-se	C 452	10.6	58.9	40	12	AAQ11990	Probe Sg918, to ena
C 380	10.6	58.9	21	22	AAI66658	Human CERP DNA rel	C 453	10.6	58.9	40	18	AAAT87125	IFN-gamma 2' F RNA
C 381	10.6	58.9	21	22	AAAF95645	Human gene single	C 454	10.6	58.9	40	20	AAAX24048	Human b7c PCR prim
C 382	10.6	58.9	21	22	AAAF97241	Human gene single	C 455	10.6	58.9	41	14	AAQ52409	Nucleic acid ligan
C 383	10.6	58.9	21	24	ABK70958	Mouse HYPLIP1 locu	C 456	10.6	58.9	41	17	AAAT07720	HIV-1 RT SELEX ide
C 384	10.6	58.9	21	24	ABK68054	Mouse HYPLIP1 locu	C 457	10.6	58.9	41	18	AAV00805	SELEX ligan 1.3c
C 385	10.6	58.9	23	14	AAQ45574	Sequence of PCR pr	C 458	10.6	58.9	41	19	AAV14590	Random region 1.3c
C 386	10.6	58.9	23	20	AAZ39452	Plasmid pSCFV31 co	C 459	10.6	58.9	41	20	AAV79665	RNA ligan sequenc
C 387	10.6	58.9	23	20	AAZ23989	Plasmid pSCFV 31 p	C 460	10.6	58.9	41	21	AAAG2765	High-affinity nucl
C 388	10.6	58.9	23	22	AAH75613	Human crn-Like gen	C 461	10.6	58.9	41	24	ABAG9918	Human TNP PCR prim
C 389	10.6	58.9	24	16	AAAT05419	Human TGF-beta1 mr	C 462	10.6	58.9	41	24	ABK61141	SELEX process nucl
C 390	10.6	58.9	24	16	AAQ75041	Human TGF-beta(1)	C 463	10.6	58.9	41	24	AA520111	Human hsp dependen
C 391	10.6	58.9	24	17	AAAT18698	CDNA3 antisense pr	C 464	10.6	58.9	42	13	AAQ35677	IL3 promoter elem
C 392	10.6	58.9	24	20	AAK35817	PCR primer for mou	C 465	10.6	58.9	42	14	AAQ50255	HIV env INS mutage
C 393	10.6	58.9	24	21	AAZ35967	Cytochrome P450 cy	C 466	10.6	58.9	42	18	AAAT47159	Primer JCA158 used
C 394	10.6	58.9	24	24	AAK93320	Ferritin 14 protei	C 467	10.6	58.9	42	18	AAAT47164	Primer JCA158 used
C 395	10.6	58.9	24	24	ABQ03479	Oligonucleotide ad	C 468	10.6	58.9	42	20	AAK31929	Human nodal DNA am
C 396	10.6	58.9	24	24	ABI82402	Capture oligonucle	C 469	10.6	58.9	42	21	AAZ47012	Primer JCA158 for
C 397	10.6	58.9	24	24	ABI82403	Capture oligonucle	C 470	10.6	58.9	42	24	ABA97892	GFP-seguroin linke
C 398	10.6	58.9	24	24	ABI91668	Capture oligonucle	C 471	10.6	58.9	43	19	AAV36942	Self-cleaving G8 D
C 399	10.6	58.9	24	24	ABI91669	Capture oligonucle	C 472	10.6	58.9	43	20	AAV84742	Antibody heavy cha
C 400	10.6	58.9	24	24	ABI92598	Capture oligonucle	C 473	10.6	58.9	44	22	AAAX77159	Rat VL30 packaging
C 401	10.6	58.9	24	24	ABI92599	Capture oligonucle	C 474	10.6	58.9	44	22	AAH23283	3x2F ZGS zinc fing
C 402	10.6	58.9	24	24	ABI92788	Capture oligonucle	C 475	10.6	58.9	45	16	AAAT01086	YJuns-rev11B cons
C 403	10.6	58.9	24	24	ABI92789	Capture oligonucle	C 476	10.6	58.9	45	16	AAO83912	Hepatitis C virus
C 404	10.6	58.9	26	19	AAV37879	PCR primer used to	C 477	10.6	58.9	45	17	AAAT16672	Hepatitis C virus
C 405	10.6	58.9	26	19	AAV35016	Primer for human C	C 478	10.6	58.9	46	22	AAH01946	parc resistance ge
C 406	10.6	58.9	26	19	AAV20685	TAR mmetic oligon	C 479	10.6	58.9	46	22	ABK52805	Human prodynorphin
C 407	10.6	58.9	26	21	AAAO8096	Riesus CD11a I-dom	C 480	10.6	58.9	47	19	AAV56425	Human ICAM-R CDNA
C 408	10.6	58.9	26	21	AAZ54653	Neisseria species	C 481	10.6	58.9	47	21	AAA97167	CDR2 nucleotide se
C 409	10.6	58.9	26	24	ABK66928	Human gene specifi	C 482	10.6	58.9	47	21	AAAO8313	Murine ICR-1.1 ant
C 410	10.6	58.9	27	16	AAAT03273	Primer DVI derived	C 483	10.6	58.9	47	21	AAZ24339	Humanised murine a
C 411	10.6	58.9	27	20	AAH81374	HIV-1 BRU tat gene	C 484	10.6	58.9	47	23	AAH88365	CNS disorder-relat
C 412	10.6	58.9	28	13	AAQ31588	PCR primer for the	C 485	10.6	58.9	49	22	AAAC91231	Human schizophren
C 413	10.6	58.9	28	20	AAZ32514	PCR primer RelB-P3	C 486	10.6	58.9	50	22	AAAL30953	Human SNP oligonuc
C 414	10.6	58.9	28	21	AAZ49427	5' primer BCK1 for	C 487	10.6	58.9	50	22	AAAL31527	Human SNP oligonuc
C 415	10.6	58.9	29	11	AAAF57337	Polymorphic fragme	C 488	10.6	58.9	50	22	AAAL34259	Human SNP oligonuc
C 416	10.6	58.9	29	11	AAAO4117	TRV93PST primer f	C 489	10.6	58.9	50	22	AAAT75587	Human silent SNP c
C 417	10.6	58.9	30	11	AAQ04634	PCR primer for tru	C 490	10.6	58.9	50	23	AAH23287	3x2F ZGL zinc fing
C 418	10.6	58.9	30	14	AAQ41177	EBP primer 386-4.	C 491	10.6	58.9	50	23	ABLO0153	Human silent nonco
C 419	10.6	58.9	30	15	AAQ63761	Beta-cardiac myosi	C 492	10.4	57.8	14	10	AAAN94504	Probe for N-termin
C 420	10.6	58.9	30	16	AAQ091122	Interleukin-12 p-3	C 493	10.4	57.8	15	16	AAAT55760	Human TNP-alpha ha
C 421	10.6	58.9	30	17	AAAT44254	eck receptor bindi	C 494	10.4	57.8	15	16	AAAT52162	Human ICAM hammerh
C 422	10.6	58.9	30	18	AAAT43766	T-cell receptor-ga	C 495	10.4	57.8	15	21	AAAG34320	C-1027 gene cluste
C 423	10.6	58.9	30	20	AAAX25301	Mouse spingostine	C 496	10.4	57.8	15	21	AAZ64230	Substrate for ham
C 424	10.6	58.9	30	21	AAZ47169	Human biallelic po	C 497	10.4	57.8	15	22	AAAF52899	IGF-I oligonucleot
C 425	10.6	58.9	31	20	AAAX06240	Human single nucle	C 498	10.4	57.8	15	22	AAAF52900	P2RY1 gene allele
C 426	10.6	58.9	31	22	AAI30081	Human single nucle	C 499	10.4	57.8	15	24	ABK09879	Human TNP-alpha ha
C 427	10.6	58.9	31	22	AAI30221	Human Bore Marrow	C 500	10.4	57.8	18	16	AAAT56721	Human cathepsin G
C 428	10.6	58.9	32	17	ABN85334	HIV-1 gp120 V3 loo	C 501	10.4	57.8	18	18	AAAT76293	Human cathepsin G
C 429	10.6	58.9	33	17	AAAT42149	HIV-1 gp120 DNA pr	C 502	10.4	57.8	18	19	AAV32491	Bovine retinaldehy
C 430	10.6	58.9	33	19	AAV00534	Human alpha-7 nico	C 503	10.4	57.8	18	20	AAZ18056	HB gene GBX 2 spec
C 431	10.6	58.9	33	20	AAAX56200	Rhesus monkey mela	C 504	10.4	57.8	18	20	AAAX54087	Human cathepsin G
C 432	10.6	58.9	33	21	AAAI5885	PCR primer for GDP	C 505	10.4	57.8	18	21	AAAF19653	Human cathepsin G
C 433	10.6	58.9	33	21	AAZ45323	Human beta-actin p	C 506	10.4	57.8	18	21	AAAG33531	Low adenosine anti
C 434	10.6	58.9	33	24	ABL57838	Human hRRTI PCR pr	C 507	10.4	57.8	19	19	AAZ55853	Bovine retinaldehy
C 435	10.6	58.9	33	24	ABK12120	Breast cancer spec	C 508	10.4	57.8	19	19	AAV57786	Human chromosome 1
C 436	10.6	58.9	34	14	AAQ52074	Acetyltransferase	C 509	10.4	57.8	20	16	AAQ82617	Chromosome 11 (loc
C 437	10.6	58.9	34	22	AAH41280	M. tuberculosis 23	C 510	10.4	57.8	20	17	AAAT32608	BKAI1 gene mapping
C 438	10.6	58.9	34	22	AAAF23029	Human silent SNP c	C 511	10.4	57.8	20	17	AAAT17537	Primer #1 for tand
C 439	10.6	58.9	35	12	AAAT78919	Herpes simplex vir	C 512	10.4	57.8	20	17	AAAT18321	BKAI1 gene mapping
C 440	10.6	58.9	37	17	AAAT47995	PCR primer REGA6E	C 513	10.4	57.8	20	19	AAV18603	Synthetic human tu
C 441	10.6	58.9	37	20	AAZ29931	Sequence of probe	C 514	10.4	57.8	20	20	AAAX32050	PCR primer used to
C 442	10.6	58.9	37	20	AAV72561	NF-AT transcriptio	C 515	10.4	57.8	20	20	AAAX33591	Oligonucleotide ta
C 443	10.6	58.9	38	14	AAAO40320	Human nuclear fact	C 516	10.4	57.8	20	21	AAAA29856	Human jun N-termin
C 444	10.6	58.9	38	16	AAO86685	T. brucei trypanos	C 517	10.4	57.8	20	21	AAAA09887	Human TNFalpha ant
C 445	10.6	58.9	38	21	AAAT29271		C 518	10.4	57.8	20	21	AAAA11139	Human TNFalpha ant
C 446	10.6	58.9	38	21	AAAI2115		C 519	10.4	57.8	20	22	AAD10590	Human MMP2 chimeri
C 447	10.6	58.9	38	21	AAAI2115		C 520	10.4	57.8	20	22	AAAD10536	REVOLUTA cDNA PCR

C 521	10.4	57.8	20	22	AAH39565	SNP specific upper	594	10.4	57.8	38	14	AAO39347	VH-CH1 repertoire
C 522	10.4	57.8	20	22	AAF94873	Human ICER4 gene p	595	10.4	57.8	38	16	AAH53833	Rat ICAM Hammerhead
523	10.4	57.8	20	24	ABK94887	Fat regulated gene p	C 596	10.4	57.8	38	21	AAAS0727	Primer TOP2-431r f
524	10.4	57.8	20	24	ABJ94349	Mouse C/EBP beta p	C 597	10.4	57.8	38	24	AAK98445	Human V gene 11bra
525	10.4	57.8	20	24	ABJ29413	Penicillium sclero	C 598	10.4	57.8	40	18	AAK97407	Synthetic oligomer
C 527	10.4	57.8	21	21	AAAC88423	Primer #1 used to	C 599	10.4	57.8	41	24	ABN89505	Human snRNP access
C 528	10.4	57.8	21	22	AAAS22644	Human COL9A1 PCR p	C 600	10.4	57.8	45	17	AAAT34003	Primer for beta ch
C 529	10.4	57.8	21	22	AAH261633	Interferon recepto	C 601	10.4	57.8	47	20	AAAX5655	Primer 28. Synthe
530	10.4	57.8	21	22	AAAF95766	Human RPS homology	C 602	10.4	57.8	50	18	AAAT61580	VH and scfv antibo
531	10.4	57.8	21	22	AAAF95820	Human gene single	C 603	10.4	57.8	50	22	AAAL29466	scfv antibody 11br
C 532	10.4	57.8	22	15	AAO65757	Type II procollase	C 604	10.4	57.8	50	22	AAAL29466	Human SNP oligonuc
C 533	10.4	57.8	22	24	ABO62255	Mouse synectin 4 i	C 605	10.4	57.8	50	22	AAAL29466	Human SNP oligonuc
534	10.4	57.8	22	24	ABR95593	Human G-protein co	C 606	10.2	56.7	16	18	AAAT92447	TAT system oligonu
535	10.4	57.8	22	13	AAO23701	Primer HUVH2ABACK	C 607	10.2	56.7	17	18	AAAT92447	Mouse f1t-1-VEGF r
536	10.4	57.8	23	13	AAO32276	Human heavy chain	C 608	10.2	56.7	17	18	AAAT92447	TAT system oligonu
537	10.4	57.8	23	14	AAO39334	VH domain PCR amp1	C 609	10.2	56.7	17	21	AAAF02559	Hammerhead ribozym
538	10.4	57.8	23	14	AAO48988	Multimeric (SBP) a	C 610	10.2	56.7	17	21	AAAF02559	Hammerhead ribozym
539	10.4	57.8	23	16	AAAT29178	HUVH2a 5' heavy ch	C 611	10.2	56.7	17	24	ABN09236	Human GDMLP-1 17-m
540	10.4	57.8	23	21	AAZ43844	Human IgG4 heavy c	C 612	10.2	56.7	17	24	ABN09237	Human GDMLP-1 17-m
541	10.4	57.8	23	22	ABAO3073	PCR primer Hu VH2-	C 613	10.2	56.7	17	24	ABN09238	Human GDMLP-1 17-m
542	10.4	57.8	23	22	AAD20056	Human antibody VH	C 614	10.2	56.7	18	18	AAAT75547	Mouse f1t-1-VEGF r
543	10.4	57.8	23	22	AAD13201	Human VH domain am	C 615	10.2	56.7	18	20	AAAT75547	Primer #34. Synth
544	10.4	57.8	23	22	AAO13301	Human VH domain am	C 616	10.2	56.7	18	21	AAAT75547	Human Smad1 antise
C 545	10.4	57.8	23	22	AAO50624	Protein kinase cdn	C 617	10.2	56.7	18	24	ABH88163	Rabbit beta-globin
546	10.4	57.8	23	23	ABN87304	Human VH domain PC	C 618	10.2	56.7	19	20	AAAX90634	Primer FIV5 to Int
547	10.4	57.8	23	24	ABK93296	Human androgen rec	C 619	10.2	56.7	19	20	AAAX37253	Human D1S7 gene sp
548	10.4	57.8	23	24	ABK93296	PCR primer #2 for	C 620	10.2	56.7	19	21	AAZ38233	HIV-1 tat gene rib
549	10.4	57.8	23	24	ABK93296	PCR primer #2 used	C 621	10.2	56.7	19	22	AAAD15493	Human NOVX7 DNA in
550	10.4	57.8	23	24	AAK98427	Human V gene 11bra	C 622	10.2	56.7	19	22	AAAD15494	Human NOVX7 DNA in
551	10.4	57.8	23	24	AAK98427	Human V gene 11bra	C 623	10.2	56.7	19	22	AAAD15494	HIV tat exon 1 o11
552	10.4	57.8	23	24	AAO30848	PCR primer HUVH2B	C 624	10.2	56.7	19	22	AAAF24107	Flexibacter mariti
553	10.4	57.8	23	24	AAZ24689	Human antibody VH	C 625	10.2	56.7	19	23	ABV10767	Human prostate exp
554	10.4	57.8	24	20	AAZ24689	Llama IgG2-specific	C 626	10.2	56.7	19	24	ABH60721	Packaging express
C 555	10.4	57.8	24	20	AAK23451	Human TRKs RACE p	C 627	10.2	56.7	20	13	AAO26641	Primer PEL. Synth
556	10.4	57.8	24	21	AAK37154	Human PEO113 reve	C 628	10.2	56.7	20	14	AAO53281	PMV primer 5' . S
C 557	10.4	57.8	24	21	AAZ24573	Non-human animal b	C 629	10.2	56.7	20	15	AAO44577	Antisense oligonuc
558	10.4	57.8	24	21	AAZ24573	Primer #8 used in	C 630	10.2	56.7	20	16	AAAT01806	Peptide nucleic ac
559	10.4	57.8	24	24	ABK67119	Human gene specific	C 631	10.2	56.7	20	17	AAAT33082	Antisense oligonuc
560	10.4	57.8	24	24	ABK67119	Oligonucleotide ad	C 632	10.2	56.7	20	18	AAAT65494	CAY immunogenic pe
561	10.4	57.8	24	24	ABO07305	Oligonucleotide ad	C 633	10.2	56.7	20	19	AAAT65494	Human telomerase r
C 562	10.4	57.8	24	24	ABO07346	Oligonucleotide ad	C 634	10.2	56.7	20	20	AAAT65494	PCR primer used to
563	10.4	57.8	25	13	AAO34326	Downstream PCR pr1	C 635	10.2	56.7	20	20	AAZ02391	PCR primer used to
C 564	10.4	57.8	25	22	AAO20181	Yeast GPR2 mutant	C 636	10.2	56.7	20	20	AAAX94146	PCR primer used to
565	10.4	57.8	25	22	AAO20182	Yeast GPR2 mutant	C 637	10.2	56.7	20	20	AAAX33586	Oligonucleotide ta
C 566	10.4	57.8	25	22	AAO20182	Yeast GPR2 mutant	C 638	10.2	56.7	20	20	AAAX33589	PCR primer for CDK
567	10.4	57.8	25	22	AAO20182	Overlapping oligon	C 639	10.2	56.7	20	20	AAAX33589	Human CDKN1A genot
C 568	10.4	57.8	25	24	AAO20182	Overlapping oligon	C 640	10.2	56.7	20	20	AAAX33589	Non-B, non-C, non-
569	10.4	57.8	26	14	AAO38382	Real-time Validat	C 641	10.2	56.7	20	21	AAAC93244	Mouse STAT3 phosph
C 570	10.4	57.8	27	12	AAO10665	Sequence of oligo	C 642	10.2	56.7	20	21	AAAC93244	Human STAT3 phosph
571	10.4	57.8	27	12	AAO10665	HLA Class II locus	C 643	10.2	56.7	20	21	AAAS7510	Trabecular meshwor
572	10.4	57.8	28	22	AAO12718	Human AHC 2H01 CDN	C 644	10.2	56.7	20	21	AAAS7510	Dog genomic marker
573	10.4	57.8	28	22	AAO12718	Human AHC 2H01 CDN	C 645	10.2	56.7	20	21	AAAS7510	TRAF6 antisense ol
574	10.4	57.8	28	22	AAO12718	Human catenin-bind	C 646	10.2	56.7	20	21	AAZ48849	Human WCAM-1 antls
575	10.4	57.8	29	20	AAO12718	Human A-Raf hamme	C 647	10.2	56.7	20	21	AAZ48849	Primer amplifying
C 576	10.4	57.8	29	21	AAO12718	Human C-Raf hamme	C 648	10.2	56.7	20	21	AAZ48849	Reverse primer spe
577	10.4	57.8	30	20	AAO12718	Primer used in con	C 649	10.2	56.7	20	22	AAO10987	Human TERT primer
578	10.4	57.8	30	20	AAO12718	N. meningitidis lb	C 650	10.2	56.7	20	22	AAO10987	Human TERT marker
579	10.4	57.8	30	20	AAO12718	N. meningitidis lb	C 651	10.2	56.7	20	22	AAO10987	Human telomerase 8 mR
C 580	10.4	57.8	30	20	AAO12718	Human NHC PCR prim	C 652	10.2	56.7	20	22	AAO12718	Human telomerase r
581	10.4	57.8	31	19	AAO12718	Human NHC PCR prim	C 653	10.2	56.7	20	22	AAO12718	Human PRO190 rever
582	10.4	57.8	31	21	AAO12718	Primer AADOPRO(+H	C 654	10.2	56.7	20	24	AAO12718	Human MEK4 antise
C 583	10.4	57.8	32	12	AAO15522	Human genomic DNA	C 655	10.2	56.7	20	24	AAO15522	hTERT sense PCR pr
C 584	10.4	57.8	32	12	AAO15522	Primer for amplifi	C 656	10.2	56.7	20	24	AAO15522	Human STAT3 antise
585	10.4	57.8	33	22	AAO15522	Human novel z1nc f	C 657	10.2	56.7	20	24	AAO15522	Human B2F transcri
586	10.4	57.8	35	22	AAO15522	Human TRFR/NGFR 14	C 658	10.2	56.7	20	24	AAO15522	hTERT mRNA primer,
587	10.4	57.8	35	22	AAO15522	Human AHC 2H01 CDN	C 659	10.2	56.7	20	24	AAO15522	Mouse STAT3 antise
588	10.4	57.8	36	16	AAO15522	Human catenin-bind	C 660	10.2	56.7	20	24	AAO15522	Human STAT3 antise
589	10.4	57.8	36	17	AAO15522	Mouse ICAM hamme	C 661	10.2	56.7	20	24	AAO15522	Capture oligonucle
590	10.4	57.8	36	17	AAO15522	Rabbit CERP HH rib	C 662	10.2	56.7	20	24	AAO15522	Capture oligonucle
591	10.4	57.8	36	20	AAO15522	Human CERP HH rib	C 663	10.2	56.7	21	12	AAO12348	3' primer p6 for R
C 592	10.4	57.8	37	22	AAO15522	Amphotropic hyperp	C 664	10.2	56.7	21	16	AAO83812	Bacteriophage T7 r
593	10.4	57.8	38	13	AAO32286	ABCI polymorphism	C 665	10.2	56.7	21	18	AAV02129	Human steroid 5-a1
							C 666	10.2	56.7	21	20	AAO80842	Osteocalcin revers

c 667	10.2	56.7	21	21	AAAB7929	Human beta-3-adren	740	10.2	56.7	30	24	ABA89600	Serial analysis of
c 668	10.2	56.7	21	21	AAZ92065	PCR primer for SST	741	10.2	56.7	30	24	ABA89601	Serial analysis of
c 669	10.2	56.7	21	22	AAI64354	PCR primer R2. Un	742	10.2	56.7	30	24	ABA89615	Serial analysis of
c 670	10.2	56.7	21	24	ABA89246	Primer 12 for sequ	743	10.2	56.7	30	20	ABA89619	Serial analysis of
c 671	10.2	56.7	21	24	AA562185	Porcine reverse PC	744	10.2	56.7	31	20	AA880152	Human beta-1,4-gal
c 672	10.2	56.7	22	19	AAV06479	Human genomic DNA	745	10.2	56.7	31	20	AA806239	Human biallelic po
c 673	10.2	56.7	23	18	AAI92594	BRCA2 cancer susc	746	10.2	56.7	31	20	AA806223	Human biallelic po
c 674	10.2	56.7	23	22	AAI75433	Codon-optimised HP	747	10.2	56.7	31	21	AA890586	Herpesvirus salmtr
c 675	10.2	56.7	23	22	AAI75433	Codon-optimised HP	748	10.2	56.7	31	21	AA890586	Human genomic DNA
c 676	10.2	56.7	23	22	AAI75433	Codon-optimised HP	749	10.2	56.7	31	22	AAI29742	Human single nucle
c 677	10.2	56.7	24	10	AA890436	Oligonucleotide pr	750	10.2	56.7	31	22	AAI29742	Human single nucle
c 678	10.2	56.7	24	17	AAI38866	Primer for dhat op	751	10.2	56.7	31	22	AAI29923	Human single nucle
c 679	10.2	56.7	24	22	AAI68134	Leptomys centrarchi	752	10.2	56.7	31	22	ABK53990	Human single nucle
c 680	10.2	56.7	24	22	AAH78894	Human ylip28 PCR	753	10.2	56.7	32	20	AA831905	Human C1CA1 gene e
c 681	10.2	56.7	24	22	AAAD08031	Rat SNORF62 recept	754	10.2	56.7	32	20	AA831908	LckBP1 mutants gen
c 682	10.2	56.7	24	22	AA801864	Cytochrome P-450 (755	10.2	56.7	32	22	AAH42185	Nucleotide sequenc
c 683	10.2	56.7	24	24	ABK48513	Human 8.8 protein	756	10.2	56.7	32	24	ABLA0396	Primer 4 relative
c 684	10.2	56.7	24	24	AA817263	Forward PCR primer	757	10.2	56.7	32	24	ABLA0221	Human G protein-co
c 685	10.2	56.7	24	24	AB182824	Capture oligonucle	758	10.2	56.7	32	24	ABK13491	DT390 mutagenic ol
c 686	10.2	56.7	24	24	AB182825	Capture oligonucle	759	10.2	56.7	33	14	AAQ44329	HrlyV-1 amplifier p
c 687	10.2	56.7	24	24	AB185156	Capture oligonucle	760	10.2	56.7	33	24	AAI72678	Homo zinc finger p
c 688	10.2	56.7	24	24	AB185157	Capture oligonucle	761	10.2	56.7	33	24	ABL50149	Human base mismatch
c 689	10.2	56.7	24	24	AB189198	Capture oligonucle	762	10.2	56.7	33	24	AA817000	Human zinc finger
c 690	10.2	56.7	24	24	AB189199	Capture oligonucle	763	10.2	56.7	33	24	ABA96618	Human alpha interf
c 691	10.2	56.7	24	24	AB192090	Capture oligonucle	764	10.2	56.7	34	14	AAQ45763	Human prostate tra
c 692	10.2	56.7	24	24	AB192091	Capture oligonucle	765	10.2	56.7	34	17	AAI14836	Human zinc finger
c 693	10.2	56.7	25	14	AAQ52333	Variant peroxidase	766	10.2	56.7	34	20	AAI10274	Human zinc finger
c 694	10.2	56.7	25	21	AAA07031	Human integrin bet	767	10.2	56.7	34	20	AAI10274	PCR primer used to
c 695	10.2	56.7	25	24	ABN14128	Human GDMLP-1 25-m	768	10.2	56.7	34	21	AA853757	Primer used to amp
c 696	10.2	56.7	25	24	ABN14129	Human GDMLP-1 25-m	769	10.2	56.7	34	21	AA853757	PCR primer SQ ID
c 697	10.2	56.7	25	24	ABN14130	Human GDMLP-1 25-m	770	10.2	56.7	34	12	AA872515	Human a1ose reduc
c 698	10.2	56.7	25	24	ABN14131	Human GDMLP-1 25-m	771	10.2	56.7	36	17	AAQ14951	Primer for amplifi
c 699	10.2	56.7	25	24	ABN14132	Human GDMLP-1 25-m	772	10.2	56.7	36	18	AAI93215	Mouse neurotactin
c 700	10.2	56.7	25	24	ABN14133	Human GDMLP-1 25-m	773	10.2	56.7	36	19	AAV42028	1,3-Propenediol de
c 701	10.2	56.7	25	24	ABN14134	Human GDMLP-1 25-m	774	10.2	56.7	36	19	AAV35770	Synthetic dhaBX PC
c 702	10.2	56.7	25	24	ABN14135	Human GDMLP-1 25-m	775	10.2	56.7	36	21	AAV35749	Synthetic dhat gen
c 703	10.2	56.7	25	24	ABN14136	Human GDMLP-1 25-m	776	10.2	56.7	36	21	AAI13477	Mouse neurotactin
c 704	10.2	56.7	25	24	ABN14137	Human GDMLP-1 25-m	777	10.2	56.7	36	21	AAI13483	Mouse neurotactin
c 705	10.2	56.7	25	24	ABN14138	Human GDMLP-1 25-m	778	10.2	56.7	36	21	AA289272	Human tissue bindi
c 706	10.2	56.7	26	24	ABK33454	Human TNF-receptor	779	10.2	56.7	36	21	AA258933	Murine neurotactin
c 707	10.2	56.7	27	14	AAQ43749	Sequence of primer	780	10.2	56.7	36	21	AA258933	Murine neurotactin
c 708	10.2	56.7	27	21	AA87921	Human beta-3-adren	781	10.2	56.7	36	22	AA238978	Expression vector
c 709	10.2	56.7	27	21	AAZ60899	Primer for geranyl	782	10.2	56.7	36	22	ABA02676	Hinge/Linker oligo
c 710	10.2	56.7	27	22	AAH75615	Human crn-1-like gen	783	10.2	56.7	36	22	ABA02677	Hinge/Linker oligo
c 711	10.2	56.7	27	24	ABK15323	PCR primer #2, use	784	10.2	56.7	36	22	AAH42579	PCR primer for DNA
c 712	10.2	56.7	27	24	ABK15764	Adenoviral vector	785	10.2	56.7	36	22	AAH73759	Human anti-human f
c 713	10.2	56.7	27	24	ABA89599	Serial analysis of	786	10.2	56.7	36	22	AAI81998	K. pneumoniae 1,3-
c 714	10.2	56.7	27	24	ABA89599	Serial analysis of	787	10.2	56.7	36	22	AAI81998	Murine neurotactin
c 715	10.2	56.7	28	14	AAQ51977	B-cell mRNA ribozy	788	10.2	56.7	36	22	AAI59267	Murine neurotactin
c 716	10.2	56.7	28	17	AAI28554	Universal bacteria	789	10.2	56.7	36	22	AAI59267	Murine neurotactin
c 717	10.2	56.7	28	17	AAI38839	Primer for dhaB3 o	790	10.2	56.7	36	22	AAI38839	Primer 1 amplifies
c 718	10.2	56.7	28	19	AAV42034	1,3-Propenediol de	791	10.2	56.7	37	17	AAI61999	E. blattae 1,3-pro
c 719	10.2	56.7	28	19	AAV35755	Synthetic dhaB/dha	792	10.2	56.7	37	20	AA866999	Humanised antibody
c 720	10.2	56.7	28	22	AAI25257	PCR primer used to	793	10.2	56.7	37	20	AAI25257	Primer pRNU6 use
c 721	10.2	56.7	28	22	ABA76949	Universal hybridis	794	10.2	56.7	38	24	AA899419	PCR primer FL5110
c 722	10.2	56.7	28	22	AAH49543	Human GTP-binding	795	10.2	56.7	38	24	ABA97259	Oligonucleotide ca
c 723	10.2	56.7	28	24	ABQ92616	Human leukaemia ch	796	10.2	56.7	38	24	ABA97260	Mutagenic primer 1
c 724	10.2	56.7	28	24	ABA89598	Serial analysis of	797	10.2	56.7	39	11	AAQ04547	T92 Guess-mer prob
c 725	10.2	56.7	28	17	ABA89609	Serial analysis of	798	10.2	56.7	39	22	AAI65803	Human IL1RA1pha ge
c 726	10.2	56.7	29	17	AAI42228	Human TBP associat	799	10.2	56.7	39	22	AAI65803	Human IL1RA1pha ge
c 727	10.2	56.7	29	17	AAI33039	Antibody L chain V	800	10.2	56.7	40	21	AAI296061	polynucleotide seq
c 728	10.2	56.7	29	17	AAI33040	Antibody L chain V	801	10.2	56.7	40	22	AAI33040	Human C-fos strept
c 729	10.2	56.7	29	17	AAI06785	Human alpha-tropom	802	10.2	56.7	40	22	AAI06785	Corn male reproduct
c 730	10.2	56.7	29	18	AAI86994	Rt-PCR primer 2 fo	803	10.2	56.7	41	21	AAI86994	Neisseria species
c 731	10.2	56.7	29	18	AAI79610	TATTA-binding prote	804	10.2	56.7	41	22	AAI79610	Human zinc finger
c 732	10.2	56.7	29	20	AAI77421	PCR primer VLAa5.	805	10.2	56.7	41	22	AAI77421	Human zinc finger
c 733	10.2	56.7	29	20	AAI77422	PCR primer VLAa5.	806	10.2	56.7	41	22	AAI77422	Human zinc finger
c 734	10.2	56.7	29	21	AAI96971	PCR primer VLAa5.	807	10.2	56.7	41	24	ABL50152	Human base mismatch
c 735	10.2	56.7	29	21	AAI96972	PCR primer VLAa5.	808	10.2	56.7	41	24	AAI96972	Human zinc finger
c 736	10.2	56.7	29	22	AAH42200	PCR primer for CDN	809	10.2	56.7	41	24	AAI96972	Human zinc finger
c 737	10.2	56.7	29	22	AAH42208	PCR primer for CDN	810	10.2	56.7	42	22	AAI96972	Plasmid pDR29 PCR
c 738	10.2	56.7	30	22	AAI69875	Erwinia herbicola	811	10.2	56.7	43	14	AAO54125	tPA insertion sequ
c 739	10.2	56.7	30	22	AAI68127	Leptomys centrarchi	812	10.2	56.7	43	14	AAO54125	tPA insertion sequ

C 813	10.2	56.7	44	19	AAV50985	Maize polymorphic	886	10	55.6	20	24	AA516603	Human inhibitor of
C 814	10.2	56.7	44	19	AAV50986	Maize polymorphic	887	10	55.6	20	24	AB143102	Human chromosome 1
C 815	10.2	56.7	44	19	AAV50991	Maize polymorphic	888	10	55.6	21	11	AAQ04708	Sequence encoding
C 816	10.2	56.7	44	19	AAV47808	Maize polymorphic	C 889	10	55.6	21	19	AAV62907	Human galactokinase
C 817	10.2	56.7	44	19	AAV47802	Maize polymorphic	C 890	10	55.6	21	21	AA545958	Polynucleotide SgQ
C 818	10.2	56.7	44	19	AAV47803	Maize polymorphic	C 891	10	55.6	21	21	AA243197	PCR primer for C.
C 819	10.2	56.7	45	14	AAQ54124	CPA insertion sequ	C 892	10	55.6	21	22	AAE97116	Human gene single
C 820	10.2	56.7	45	14	AAQ54128	CPA insertion sequ	C 893	10	55.6	21	22	AAE70506	Human DRD2 fragmen
C 821	10.2	56.7	45	21	AA337282	Human PRO1491 hybr	C 894	10	55.6	21	24	AAE71180	Human gene single
C 822	10.2	56.7	45	21	AA330323	Oligonucleotide IG	C 895	10	55.6	22	22	AAH264170	Mouse #2 used to
C 823	10.2	56.7	45	22	AAH93874	Human prostate cdn	C 896	10	55.6	22	24	ABK88730	Mouse YB-1 anti-se
C 824	10.2	56.7	45	22	AAH93874	Human prostate cdn	C 897	10	55.6	23	24	ABK88730	Mouse YB-1 anti-se
C 825	10.2	56.7	45	22	AAH93874	Human prostate cdn	C 898	10	55.6	23	24	ABK88730	Mouse YB-1 anti-se
C 826	10.2	56.7	45	20	ABA98626	Human map-related	C 899	10	55.6	23	24	ABK88730	Mouse YB-1 anti-se
C 827	10.2	56.7	46	20	ABA98626	Human map-related	C 900	10	55.6	23	24	ABK88730	Mouse YB-1 anti-se
C 828	10.2	56.7	46	20	ABA98626	Human map-related	C 901	10	55.6	23	24	ABK88730	Mouse YB-1 anti-se
C 829	10.2	56.7	46	21	AA542803	Human map-related	C 902	10	55.6	23	24	ABK88730	Mouse YB-1 anti-se
C 830	10.2	56.7	47	21	AA265874	Human map-related	C 903	10	55.6	23	24	ABK88730	Mouse YB-1 anti-se
C 831	10.2	56.7	47	21	AA265874	Human map-related	C 904	10	55.6	24	14	AAO27338	PCR primer SEQ ID
C 832	10.2	56.7	47	21	AA265874	Human map-related	C 905	10	55.6	24	14	AAO27338	Probe for HLA-DRb
C 833	10.2	56.7	47	21	AA265874	Human map-related	C 906	10	55.6	24	16	AAO46311	DR8 oligonucleotid
C 834	10.2	56.7	47	21	AA265874	Human map-related	C 907	10	55.6	24	18	AAE54893	Hepatitis C virus
C 835	10.2	56.7	47	21	AA265874	Human map-related	C 908	10	55.6	24	18	AAE54893	Hepatitis C virus
C 836	10.2	56.7	47	21	AA265874	Human map-related	C 909	10	55.6	24	20	AAE54893	Hepatitis C virus
C 837	10.2	56.7	47	21	AA265874	Human map-related	C 910	10	55.6	24	21	AAE54893	Hepatitis C virus
C 838	10.2	56.7	47	21	AA265874	Human map-related	C 911	10	55.6	24	22	AAE54893	Hepatitis C virus
C 839	10.2	56.7	47	21	AA265874	Human map-related	C 912	10	55.6	24	22	AAE54893	Hepatitis C virus
C 840	10.2	56.7	48	21	AA265874	Human map-related	C 913	10	55.6	24	22	AAE54893	Hepatitis C virus
C 841	10.2	56.7	48	21	AA265874	Human map-related	C 914	10	55.6	24	22	AAE54893	Hepatitis C virus
C 842	10.2	56.7	50	21	AA265874	Human map-related	C 915	10	55.6	24	24	AB183640	Human HLA-DR B1 ge
C 843	10.2	56.7	50	22	AA265874	Human map-related	C 916	10	55.6	24	24	AB183640	Human HLA-DR B1 ge
C 844	10.2	56.7	50	22	AA265874	Human map-related	C 917	10	55.6	25	14	AAQ47109	Human HLA-DR B1 ge
C 845	10.2	56.7	50	22	AA265874	Human map-related	C 918	10	55.6	25	14	AAQ47109	Human HLA-DR B1 ge
C 846	10.2	56.7	50	22	AA265874	Human map-related	C 919	10	55.6	25	19	AAV40933	Human HLA-DR B1 ge
C 847	10.2	56.7	50	22	AA265874	Human map-related	C 920	10	55.6	25	21	AAV40933	Human HLA-DR B1 ge
C 848	10.2	56.7	50	22	AA265874	Human map-related	C 921	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 849	10.2	56.7	50	22	AA265874	Human map-related	C 922	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 850	10.2	56.7	50	22	AA265874	Human map-related	C 923	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 851	10.2	56.7	50	22	AA265874	Human map-related	C 924	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 852	10.2	56.7	50	22	AA265874	Human map-related	C 925	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 853	10.2	56.7	50	22	AA265874	Human map-related	C 926	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 854	10.2	56.7	50	22	AA265874	Human map-related	C 927	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 855	10.2	56.7	50	22	AA265874	Human map-related	C 928	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 856	10.2	56.7	50	22	AA265874	Human map-related	C 929	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 857	10.2	56.7	50	22	AA265874	Human map-related	C 930	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 858	10.2	56.7	50	22	AA265874	Human map-related	C 931	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 859	10.2	56.7	50	22	AA265874	Human map-related	C 932	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 860	10.2	56.7	50	22	AA265874	Human map-related	C 933	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 861	10.2	56.7	50	22	AA265874	Human map-related	C 934	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 862	10.2	56.7	50	22	AA265874	Human map-related	C 935	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 863	10.2	56.7	50	22	AA265874	Human map-related	C 936	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 864	10.2	56.7	50	22	AA265874	Human map-related	C 937	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 865	10.2	56.7	50	22	AA265874	Human map-related	C 938	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 866	10.2	56.7	50	22	AA265874	Human map-related	C 939	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 867	10.2	56.7	50	22	AA265874	Human map-related	C 940	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 868	10.2	56.7	50	22	AA265874	Human map-related	C 941	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 869	10.2	56.7	50	22	AA265874	Human map-related	C 942	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 870	10.2	56.7	50	22	AA265874	Human map-related	C 943	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 871	10.2	56.7	50	22	AA265874	Human map-related	C 944	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 872	10.2	56.7	50	22	AA265874	Human map-related	C 945	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 873	10.2	56.7	50	22	AA265874	Human map-related	C 946	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 874	10.2	56.7	50	22	AA265874	Human map-related	C 947	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 875	10.2	56.7	50	22	AA265874	Human map-related	C 948	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 876	10.2	56.7	50	22	AA265874	Human map-related	C 949	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 877	10.2	56.7	50	22	AA265874	Human map-related	C 950	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 878	10.2	56.7	50	22	AA265874	Human map-related	C 951	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 879	10.2	56.7	50	22	AA265874	Human map-related	C 952	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 880	10.2	56.7	50	22	AA265874	Human map-related	C 953	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 881	10.2	56.7	50	22	AA265874	Human map-related	C 954	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 882	10.2	56.7	50	22	AA265874	Human map-related	C 955	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 883	10.2	56.7	50	22	AA265874	Human map-related	C 956	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 884	10.2	56.7	50	22	AA265874	Human map-related	C 957	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge
C 885	10.2	56.7	50	22	AA265874	Human map-related	C 958	10	55.6	25	24	ABO64492	Human HLA-DR B1 ge

C 959	10	55.6	25	24	ABN14143	Human GDM1P-1 25-m
C 960	10	55.6	25	24	ABN14144	Human GDM1P-1 25-m
C 961	10	55.6	26	25	AAV16265	Dual labeled fluor
C 962	10	55.6	26	22	AAV11183	Human beta-globin
C 963	10	55.6	26	22	AAH45992	Human beta-globin
C 964	10	55.6	26	22	AAV59149	Dual-labeled fluor
C 965	10	55.6	26	22	AAV59149	Dual-labeled fluor
C 966	10	55.6	26	22	AAV59149	Dual-labeled fluor
C 967	10	55.6	26	22	AAV59149	Dual-labeled fluor
C 968	10	55.6	27	14	AAQ41722	HBV polyA sequence
C 969	10	55.6	27	14	AAQ41722	PCR primer to ampl
C 970	10	55.6	27	14	AAQ41722	Encodes C-terminus
C 971	10	55.6	27	14	AAQ41722	MI primer (1). Sy
C 972	10	55.6	27	14	AAQ41722	Primer B1 of the i
C 973	10	55.6	28	16	AAV01011	HBV polyA sequence
C 974	10	55.6	28	16	AAV01011	Modified human lym
C 975	10	55.6	28	21	AAZ58564	Ink4a-p16 specific
C 976	10	55.6	28	22	AAH47826	Mouse Ink4a-p16 se
C 977	10	55.6	28	22	AAH47826	RT PCR primer 1.
C 978	10	55.6	29	4	AAH30137	Human p53 binding
C 979	10	55.6	29	14	AAQ52822	Sequence of DNA tr
C 980	10	55.6	29	14	AAQ52823	HCV target sequenc
C 981	10	55.6	29	15	AAQ82941	Human mutated PIP
C 982	10	55.6	29	16	AAQ79812	Hepatitis C virus
C 983	10	55.6	29	16	AAQ79812	HSV L/ST ORF3. He
C 984	10	55.6	29	18	AAH89682	Probe used in the
C 985	10	55.6	29	20	AAH19522	Integrin alpha 6 s
C 986	10	55.6	29	20	AAZ07634	HCV J1 isolate NS1
C 987	10	55.6	29	20	AAZ06784	PCR primer and pro
C 988	10	55.6	29	20	AAZ00448	Hepatitis C virus
C 989	10	55.6	29	21	AAV92103	Human A-Raf hamme
C 990	10	55.6	29	21	AAV92103	Hammerhead ribozym
C 991	10	55.6	29	21	AAH30369	Plasmid TKH2 PCR
C 992	10	55.6	29	21	AAH30369	Polymorphic fragme
C 993	10	55.6	29	21	AAH30369	Polymorphic fragme
C 994	10	55.6	29	21	AAH30369	Primer used in PC
C 995	10	55.6	29	24	AAZ58442	3' HBV polymerase
C 996	10	55.6	30	10	AAH92580	Wild type sequence
C 997	10	55.6	30	10	AAH92581	Gln4 mutant sequen
C 998	10	55.6	30	16	AAQ93259	Family 1A bFGF 2'-
C 999	10	55.6	30	21	AAH84861	Human endonuclease
C1000	10	55.6	30	21	AAH53082	Rat genomic DNA ve
					AAZ88251	Treponema pallidum

ALIGNMENTS

```

RESULT 1
AAS19106
ID AAS19106 standard; DNA; 18 BP.
XX
XX AAS19106;
AC
XX
XX 15-MAR-2002 (first entry)
DT
XX
XX Human p53 coding sequence antisense sequence SEQ ID NO: 35.
DE
XX
XX Antisense; splice region; mRNA splice processing inhibition;
XX splice variant; protein expression inhibition; human; HIV-1; rat; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200183740-A2.
PN
XX
XX 08-NOV-2001.
PD
XX
XX 04-MAY-2001; 2001WO-US14410.
PF
XX
XX 04-MAY-2000; 2000US-202376P.
PR
XX
XX (AVIB-) AVI BIOPHARMA INC.
PA
XX
XX Iversen PL, Hudziak R;
PI

```

```

XX
XX WPI; 2002-066533/09.
DR
XX
XX Splice-region antisense composition and method
PT
XX
XX Claim 18; Page 23; 53pp; English.
PS
XX
XX The present invention relates to antisense compositions targeted to an
CC mRNA sequence for a selected protein, at a region having its 5' end from
CC 1 to about 25 base pairs downstream of a normal splice acceptor junction
CC in the preprocessed mRNA. The antisense compound is RNase-inactive, and
CC is preferably a phosphorodiamidate-linked morpholino oligonucleotide.
CC Such targeting is effective to inhibit natural mRNA splice processing,
CC produce splice variant mRNAs, and inhibit normal expression of the
CC protein. The present sequence is an antisense sequence described in the
CC exemplification of the invention.
XX
SQ Sequence 18 BP; 3 A; 6 C; 7 G; 2 T; 0 other;

```

```

Query Match 100.0%; Score 18; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CCCGGAAGCAGCTGCG 18
Db 1 CCCGGAAGCAGCTGCG 18

```

```

RESULT 2
AAS19107
ID AAS19107 standard; DNA; 36 BP.
XX
XX AAS19107;
AC
XX
XX 15-MAR-2002 (first entry)
DT
XX
XX Human p53 coding sequence antisense sequence SEQ ID NO: 36.
DE
XX
XX Antisense; splice region; mRNA splice processing inhibition;
XX splice variant; protein expression inhibition; human; HIV-1; rat; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200183740-A2.
PN
XX
XX 08-NOV-2001.
PD
XX
XX 04-MAY-2001; 2001WO-US14410.
PF
XX
XX 04-MAY-2000; 2000US-202376P.
PR
XX
XX (AVIB-) AVI BIOPHARMA INC.
PA
XX
XX Iversen PL, Hudziak R;
PI
XX
XX WPI; 2002-066533/09.
DR
XX
XX Splice-region antisense composition and method
PT
XX
XX Claim 37; Page 23; 53pp; English.
PS
XX
XX The present invention relates to antisense compositions targeted to an
CC mRNA sequence for a selected protein, at a region having its 5' end from
CC 1 to about 25 base pairs downstream of a normal splice acceptor junction
CC in the preprocessed mRNA. The antisense compound is RNase-inactive, and
CC is preferably a phosphorodiamidate-linked morpholino oligonucleotide.
CC Such targeting is effective to inhibit natural mRNA splice processing,
CC produce splice variant mRNAs, and inhibit normal expression of the
CC protein. The present sequence is an antisense sequence described in the
CC exemplification of the invention.
XX
SQ Sequence 36 BP; 6 A; 11 C; 12 G; 7 T; 0 other;

```

Query Match 100.0%; Score 18; DB 24; Length 36;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGTGCG 18
 |||||||||||||||
 DB 17 CCCGGAAGCAGCTGTGCG 34

RESULT 3
 AAX26511/c
 ID AAX26511 standard; DNA; 37 BP.
 XX
 AC AAX26511;
 XX
 DT 28-MAY-1999 (first entry)
 XX
 DE WO 9909191 SeqID #13.
 XX
 XX Cancer; treatment; vector; recombinase gene; transcription factor;
 KM selective cell killing; gene therapy; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9909191-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 02-JUL-1998; 98WO-JP02993.
 XX
 PR 20-AUG-1997; 97JP-0223651.
 XX
 PA (DNMV-) DNAVEC RES INC.
 XX
 PI Hasegawa M, Takeda K, Yokoi H;
 XX
 DK WPI; 1999-181048/15.
 XX
 PT Gene expression specific to cells free from specific transcription
 PT factor with constructed recombinase expression unit after infecting
 PT cells - allowing expression of target gene in gene therapy.
 PT particularly in cancer treatment
 PS Example 1; Page 16; 49pp; Japanese.
 XX
 CC This invention describes a vector containing a recombinase gene which
 CC is controlled by (1) a promoter and action of which is in turn dependent
 CC on a specific transcription factor and (2) a desired gene to be expressed
 CC and two target sequences of the recombinase. Also described in the
 CC invention are (1) a host cell for introduction of the vector and (11) an
 CC in vitro technique in which killing of cells without the specific
 CC transcription factor is selectively performed after the vector is
 CC introduced into a host cell by an in vitro technique. The technique is
 CC used for gene therapy e.g. in cancer treatment. The products of the
 CC invention allow the use of a specific vector specifically and safely,
 CC there is little toxicity.
 CC
 SO Sequence 37 BP; 7 A; 13 C; 9 G; 8 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 37;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGTGCG 18
 |||||||||||||||
 DB 30 CCCGGAAGCAGCTGTGCG 13

RESULT 4
 AAG61823/c
 ID AAG61823 standard; DNA; 25 BP.
 XX
 AC AAG61823;

XX
 XX 19-SEP-1994 (first entry)
 XX
 DE Primer for mutant p53 sequence.
 XX
 DE Fragment A: RGC; transcriptional regulator; TR; germ line mutation;
 KM assay; cancer; PCR; amplification; sense; ss.
 XX
 OS Synthetic.
 XX
 PN WO9408049-A.
 XX
 PD 14-APR-1994.
 XX
 PF 28-SEP-1993; 93WO-US09259.
 XX
 PR 01-OCT-1992; 92US-0956696.
 XX
 PR 12-APR-1993; 93US-0046033.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PA (SURE-) INST SUISSE RECH EXPERIMENTALE.
 XX
 PI Frebourg T, Friend SH, Iggo R, Ishioka C;
 XX
 DR WPI; 1994-135609/16.
 XX
 PT Assay for mutations in a transcriptional regulator gene - using
 PT cells transfected with the gene and DNA encoding a detectable
 PT protein expressed in response to the gene.
 PS Example; Page 21; 51pp; English.
 XX
 CC The sequence is that of a sense PCR primer for amplification of a
 CC mutant p53 gene. The PCR prod. can be used in an assay to directly
 CC assess whether a germ-line mutation in a gene which is a trans-
 CC criptional regulator results in the prod. of a non functional gene.
 CC This may be used in screening individuals at risk of cancer or in cancer
 CC prognosis.
 CC See also AAG61818-24.
 XX
 SO Sequence 25 BP; 4 A; 8 C; 7 G; 6 T; 0 other;

Query Match 83.3%; Score 15; DB 15; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAAGCAGCTGTGCG 18
 |||||||||||
 DB 25 GGAAGCAGCTGTGCG 11

RESULT 5
 AAC86956/c
 ID AAC86956 standard; DNA; 26 BP.
 XX
 AC AAC86956;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE PCR primer used to amplify a fragment of DNA encoding p53.
 XX
 DE Antitumor; antiviral; p53; cytotoxic polypeptide; immune response;
 KM tumour; virus-infected cell; proliferative disease; restenosis;
 KM viral infection; hepatitis; herpes; PCR primer; ss.
 XX
 OS unidentified.
 XX
 PN WO200071078-A2.
 XX
 PD 30-NOV-2000.
 XX
 PF 25-MAY-2000; 2000WO-FR01422.
 XX

```

PR 25-MAY-1999; 99FR-0006892.
PA (TRGE ) TRANSGENE.
PI Erbs P, Jund R;
XX WPI: 2001-061278/07.
XX Composition containing p53 gene and gene for cytotoxin, useful for
PT treating tumours and viral infections, with synergistic activity
XX
XX Example 1; Page 32; 58pp; French.
XX
CC The specification describes a composition for use as antitumor or
CC antiviral agent in mammals. The composition comprises a sequence
CC encoding all or part of p53 and at least one sequence encoding all or
CC part of a cytotoxic polypeptide. These sequences are under control of
CC suitable expression elements. There is a synergistic increase in activity
CC when p53 and the cytotoxic polypeptide are used together, with improved
CC presentation of antigens and/or stimulation of the host's immune cells.
CC The composition is used for the induction and activation of an immune
CC response specific for tumours or virus-infected cells, or inhibition of
CC growth and division (preferably killing) of such cells. The composition
CC is used to treat or prevent tumours (or other proliferative diseases,
CC e.g. restenosis) and viral infections (e.g. caused by hepatitis B or C,
CC herpes of human immune deficiency virus), in humans and animals. PCR
CC primers AAC86956-57 were used to amplify a fragment of DNA encoding p53
CC protein.
XX
S0 Sequence 26 BP; 5 A; 9 C; 7 G; 5 T; 0 other;
XX
Query Match 82.2%; Score 14.8; DB 22; Length 26;
Best Local Similarity 88.9%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CCCGGAGGACGTCGGC 18
| | | | | | | | | | | | | | | | | | | |
DB 22 CCCGGAGGAAATTCTGCC 5
XX
RESULT 6
AAL42029
ID AAL42029 standard; DNA; 21 BP.
XX
AC AAL42029;
XX
DT 16-MAY-2002 (first entry)
XX
DE T. reesei endoglucanase III cellulase mutagenic reverse PCR primer H450.
XX
XX Mutagenic PCR; primer; H450; variant endoglucanase III cellulase;
KW variant EsIII cellulase; temperature stress resistant; textile treatment;
KW wood pulp treatment; biomass to glucose reduction; ss;
XX indigo dyed denim stone washing; feed additive.
XX
OS Trichoderma reesei.
OS Synthetic.
OS
XX WO200212463-A2.
XX
PN 14-FEB-2002.
PD
XX 31-JUL-2001; 2001WO-US23960.
XX
PF 04-AUG-2000; 2000US-0632575.
XX
PR (GENV ) GENENCOR INT INC.
XX
PA Gualfetti P, Mitchinson C, Ropp TH;
PI WPI: 2002-241749/29.
XX
DR New variant endoglucanase III cellulase useful in treatment of
PT

```

PT cellulose containing textile, in the reduction of biomass to glucose
PT and as feed additive, has substitution at a residue sensitive to
PT temperature stress -
XX
XX Example 1; Page 28; 40pp; English.
XX
CC The invention comprises variant Trichoderma reesei endoglucanase III
CC (EgIII) cellulases which are more resistant to temperature stress than
CC wild type EgIII cellulase. The variant EgIII cellulases of the invention
CC are useful in the treatment of a cellulase containing textile, the
CC treatment of wood pulp, in the reduction of biomass to glucose, stone
CC washing of indigo dyed denim, and as a feed additive. The present
CC nucleotide sequence represents a mutagenic PCR primer used in the
CC production of a variant EgIII cellulase of the invention.
XX
S0 Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 other;

Query Match 73.3%; Score 13.2; DB 24; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCGAGCAGCATCTGGC 18
||| ||||||| |||||
Db 4 CCTGCAGCACACTGGC 21

RESULT 7
AAL42028/c
ID AAL42028 standard; DNA; 27 BP.
XX
AC AAL42028;
XX
DT 16-MAY-2002 (first entry)
XX
DE T. reesei endoglucanase III cellulase mutagenic forward PCR primer H450.
XX
XX Mutagenic PCR primer; H450; variant endoglucanase III cellulase;
KW variant EgIII cellulase; temperature stress resistant; textile treatment;
RW wood pulp treatment; biomass to glucose reduction; ss;
KW indigo dyed denim stone washing; feed additive.
XX
OS Trichoderma reesei.
OS Synthetic.
XX
PN WO200212463-A2.
XX
PD 14-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US23960.
XX
PR 04-AUG-2000; 2000US-0632575.
PA (GENV) GENENCOR INT INC.
XX
PI Gualfetti P, Mitchinson C, Ropp TH;
XX WPI: 2002-241749/29.
DR
XX
XX New variant endoglucanase III cellulase useful in treatment of
PT cellulose containing textile, in the reduction of biomass to glucose
PT and as feed additive, has substitution at a residue sensitive to
PT temperature stress -
XX
XX Example 1; Page 28; 40pp; English.
XX
CC The invention comprises variant Trichoderma reesei endoglucanase III
CC (EgIII) cellulases which are more resistant to temperature stress than
CC wild type EgIII cellulase. The variant EgIII cellulases of the invention
CC are useful in the treatment of a cellulase containing textile, the
CC treatment of wood pulp, in the reduction of biomass to glucose, stone
CC washing of indigo dyed denim, and as a feed additive. The present
CC nucleotide sequence represents a mutagenic PCR primer used in the
CC production of a variant EgIII cellulase of the invention.

CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CERP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CERP mRNA. As the ribozymes
CC target specific regions of the CERP gene, they have low non-specific
CC activity.

XX
SQ Sequence 18 BP; 3 A; 8 C; 5 G; 2 U; 0 other;

Query Match 71.1%; Score 12.8; DB 17; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CCGAAGCAGCTCTGG 17
| | | | | | | | | | | | | | | | | |
DB 16 CTGGAAGCGCTCTGG 1

RESULT 10
AA092447/c
ID AA092447 standard; DNA; 28 BP.

XX
AC AA092447;
XX
DT 11-JAN-1996 (first entry)
XX

DE CD3 delta chain 3' PCR detection primer.

XX
KW Primer; PCR; amplification; natural killer cell; purification; CD3; CD5;
KW antibody; interleukin; proliferation; target cell type; beta-actin;
KW allogenic lymphoblastoid; T-cell receptor; gene expression; ss.

OS Synthetic.

XX
PN US5415874-A.

XX
PD 16-MAY-1995.

XX
PF 31-OCT-1989; 89US-0429353.

XX
PR 31-OCT-1989; 89US-0429353.

XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX
PI Bender JR, Engleman EG, Parol R;

XX
DR WPI: 1995-193394/25.

XX
PT Prodn. of target cell-specific natural killer cells - by selecting
PT natural killer cells based on their adhesion to a selected target
PT cell type and culturing.

XX
PS Example 5; Column 15; 23pp; English.

CC Primers AA092434-49 were used to PCR detect specific messenger RNAs in
CC cultured natural killer (NK) cells. The NK cells are purified by
CC partial purification through a nylon wool column followed by removal
CC of the CD3+ and CD5+ cells by incubating in the presence of bound
CC anti-CD3 and anti-CD5 antibodies. The remaining cells which express
CC the Leu11c+ (CD16) and Leu19 markers are enriched by propagating in a
CC medium containing an agent e.g. interleukin (IL)-2 which promotes
CC proliferation of the NK cells and in the presence of the NK cells'
CC target cell type e.g. allogenic lymphoblastoid cells.
CC Confirmation of the correct NK cell type is carried by PCR amplification
CC of the CD3 and T-cell receptor (TCR) markers alpha, beta, gamma and
CC delta, on reverse transcribed RNA isolated from the NK cells. The
CC primers AA092446-7 target the CD3 gene delta chain.

XX
SQ Sequence 28 BP; 6 A; 11 C; 6 G; 5 T; 0 other;

Query Match 71.1%; Score 12.8; DB 16; Length 28;

Best Local Similarity 87.5%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CCGAAGCAGCTCTGG 17
| | | | | | | | | | | | | | | | | |
DB 26 CTGGAAGCGCTCTGG 11

RESULT 11
AA006064
ID AA006064 standard; DNA; 30 BP.

XX
AC AA006064;

XX
DT 24-JAN-1991 (first entry)

DE N-terminus probe used to isolate p150,95 cell surface adhesion
DE receptor.

XX
KW Rhinovirus; ICAM-1; LFA-1 glycoprotein; multiple sclerosis;
KW ulcerative colitis; transplant rejection; ss.

OS Synthetic.

XX
PN WO9010646-A.

XX
PD 20-SEP-1990.

XX
PF 09-MAR-1990; 90WO-US01257.

XX
PR 09-MAR-1990; 90WO-US01257.

XX
PA (DANA-) DANA FARMER CANCER.

XX
PI Corbi AA, Springer TA;

XX
DR WPI: 1990-304985/40.

XX
PT Treatment of viral esp. rhino-viral infection - by admin. of
PT alpha sub-unit of p150,95 cell surface adhesion receptor. opt.
PT together with a beta chain of CD-18 family

XX
PS Example 1; Page 33; 59pp; English.

CC Probe was used to isolate p150,95 surface adhesion receptor from
CC hairy cell leukemia spleens by Mab affinity chromatography.
CC The isolated receptor prevents viral (particularly rhino-viral) cell-
CC virus adhesion by interacting with ICAM-1. It is useful in treatment
CC of delayed hypersensitivity, multiple sclerosis, transplant
CC rejection, ulcerative colitis etc. Abs against the receptor may be
CC used as antiinflammatory agents.

XX
SQ Sequence 30 BP; 7 A; 10 C; 9 G; 4 T; 0 other;

Query Match 71.1%; Score 12.8; DB 11; Length 30;
Best Local Similarity 87.5%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCGGAAGCAGCTCTG 16
| | | | | | | | | | | | | | | | | |
DB 12 CCGGAAGCAGCTCTGAG 27

RESULT 12

AA050604/c
ID AA050604 standard; RNA; 18 BP.

XX
AC AA050604;

XX
DT 10-MAR-1997 (first entry)

XX
DE Human CERP hairpin ribozyme target sequence #276.

KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
 KW familial hypercholesterolemia; dyslipidaemia; hypolipidoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angiolipastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KW LDL; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09620279-A1.
 XX
 PD 04-JUL-1996.
 XX
 PF 11-DEC-1995; 95WO-US16000.
 XX
 PR 23-DEC-1994; 94US-0363240.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
 DR WPI; 1996-321852/32.
 XX
 PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
 PT - useful for preventing or treating initial development, progression
 PT or regression of vascular diseases, esp. familial
 PT hypercholesterolaemia
 XX
 PS Claim 4; Page 52; 72pp; English.
 XX
 CC AAT50595-T50642 represent target sequences for the human cholesterol
 CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50599).
 CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
 CC between plasma lipoproteins. The numbering of the targets refers to the
 CC position of the cleavage site in full length CETP. The ribozyme then
 CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
 CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
 CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
 CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
 CC eliminated) thereby preventing the reduction in size density of the high
 CC density lipoproteins (HDL), prolonging HDL half life, and therefore
 CC increasing HDL levels. The ribozymes can be used to treat conditions
 CC associated with abnormal levels of CETP, specifically atherosclerosis,
 CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
 CC familial hypercholesterolaemia, hypolipidoproteinaemia, vascular
 CC complications of diabetes, transplant, atherectomy and angiolipastic
 CC restenosis. By inhibiting CETP, the levels of HDL and low density
 CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
 CC decrease in LDL levels, and a corresponding increase in HDL levels). The
 CC ribozymes can also be used diagnostically to study genetic drift and
 CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
 CC target specific regions of the CETP gene, they have low non-specific
 CC activity.
 CC
 XX
 SQ Sequence 18 BP; 3 A; 8 C; 3 G; 4 U; 0 other;
 XX
 QY Query Match 68.9%; Score 12.4; DB 17; Length 18;
 XX Best Local Similarity 92.9%; Pred. No. 7.3e+03;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 Db 4 GGAAGCGACTGTGG 17
 18 GGAAGCGCGTGTGG 5
 XX
 RESULT 13
 AAT50700/c
 ID AAT50700 standard; RNA: 18 BP.
 XX
 AC AAT50700;
 XX

DT 07-MAR-1997 (first entry)
 XX
 DE Rabbit CETP hairpin ribozyme target sequence #98.
 XX
 KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
 KW familial hypercholesterolemia; dyslipidaemia; hypolipidoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angiolipastic restenosis; low density lipoprotein; diabetes; HDL; rabbit;
 KW LDL; ss.
 KW
 XX
 OS Oryctolagus cuniculus.
 XX
 PN W09620279-A1.
 XX
 PD 04-JUL-1996.
 XX
 PF 11-DEC-1995; 95WO-US16000.
 XX
 PR 23-DEC-1994; 94US-0363240.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
 DR WPI; 1996-321852/32.
 XX
 PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
 PT - useful for preventing or treating initial development, progression
 PT or regression of vascular diseases, esp. familial
 PT hypercholesterolaemia
 XX
 PS Claim 4; Page 54; 72pp; English.
 XX
 CC AAT50699-T50754 represent target sequences for the rabbit cholesterol
 CC ester transfer protein (CETP) hairpin ribozymes (see AAT50643-T50698).
 CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
 CC between plasma lipoproteins. The numbering of the targets refers to the
 CC position of the cleavage site in full length CETP. The ribozyme then
 CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
 CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
 CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
 CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
 CC eliminated) thereby preventing the reduction in size density of the high
 CC density lipoproteins (HDL), prolonging HDL half life, and therefore
 CC increasing HDL levels. The ribozymes can be used to treat conditions
 CC associated with abnormal levels of CETP, specifically atherosclerosis,
 CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
 CC familial hypercholesterolaemia, hypolipidoproteinaemia, vascular
 CC complications of diabetes, transplant, atherectomy and angiolipastic
 CC restenosis. By inhibiting CETP, the levels of HDL and low density
 CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
 CC decrease in LDL levels, and a corresponding increase in HDL levels). The
 CC ribozymes can also be used diagnostically to study genetic drift and
 CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
 CC target specific regions of the CETP gene, they have low non-specific
 CC activity.
 CC
 XX
 SQ Sequence 18 BP; 2 A; 7 C; 5 G; 4 U; 0 other;
 XX
 QY Query Match 68.9%; Score 12.4; DB 17; Length 18;
 XX Best Local Similarity 92.9%; Pred. No. 7.3e+03;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 Db 4 GGAAGCGACTGTGG 17
 18 GGAAGCGCGTGTGG 5
 XX
 RESULT 14
 AAA87923/c

ID	AAA87923	standard; DNA; 26 BP.
XX		
AC	AAA87923;	
XX		
DT	07-DEC-2000	(first entry)
XX		
DE	Human beta-3-adrenergic receptor promoter PCR primer SEQ ID NO:22.	
XX		
KW	Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter; regulation; identification; trans-activating factor; drug screening;	
KW	gene expression regulation; obesity; type II diabetes; PCR primer; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200044901-A1.	
PD	03-AUG-2000.	
XX		
PF	01-FEB-2000; 2000WO-US02632.	
XX		
PR	01-FEB-1999; 99US-0243335.	
XX		
PA	(AMHP) AMERICAN HOME PROD CORP.	
XX		
PI	Susulic VS. Duzic E;	
DR	WPI; 2000-482973/42.	
XX		
PT	New isolated nucleic acid useful for screening assays to identify	
PT	compounds capable of regulating beta3-AR (adrenergic receptor)	
PT	expression, is composed of three regulatory segments	
XX		
PS	Example 1; Page 34; 88pp; English.	
XX		
CC	The present invention describes a core nucleotide sequence from the	
CC	B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory	
CC	region. The core nucleotide sequence binds to a B-segment-binding	
CC	trans-activating factor. Recombinant vectors under control of the	
CC	transcription regulation region comprising nucleotide sequences	
CC	containing the core nucleotide sequence from the B segment of the human	
CC	beta-3-AR regulatory region provide a substrate for high throughput	
CC	assays, particularly reporter gene assays to identify compounds capable	
CC	of increasing or decreasing the level of expression of beta-3-AR. The	
CC	nucleotide sequences can be used for regulating gene expression and for	
CC	drug screening. It is envisaged that beta-3-AR stimulation may have	
CC	beneficial effects in the treatment of obesity and type II diabetes.	
CC	The present sequence represents a PCR primer for the human beta-3-AR	
CC	promoter, which is used in an example from the present invention.	
XX		
SQ	Sequence 26 BP; 3 A; 11 C; 5 G; 7 T; 0 other;	
	Query Match	68.9%; Score 12.4; DB 21; Length 26;
	Best Local Similarity	92.9%; Pred. No. 7.4e+03;
	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
OY	5 GAAGGCAGCTCTGGC 18	
Db	24 GAAGCAGACTGGC 11	
RESULT 15		
ID	ABK33460/C	
XX	ABK33460 standard; DNA; 17 BP.	
AC	ABK33460;	
XX		
DT	23-APR-2002 (first entry)	
XX		
DE	Human TNF-receptor II 3'UNT nt 1663 (G/A) reverse PCR primer.	
XX		
KW	Human; anti-tumour necrosis factor receptor II; TNF receptor II;	
KW	TNF receptor I; Infliximab therapy; Crohn's disease; malignant disorder;	
KW	Inflammatory disorder; chronic disease; receptor; primer; ss.	

```

XX OS Homo sapiens.
XX PN EP1172444-A1.
XX PD 16-JAN-2002.
XX PF 10-JUL-2000; 2000EP-0114786.
XX PR 10-JUL-2000; 2000EP-0114786.
XX PA (CONA-) CONARIS RES INST GMBH.
XX PI Schreiber S, Hampe J, Mascheretti S;
XX WPI: 2002-156651/21.
XX
XX PR Detecting non-responders to anti-human necrosis factor therapy,
XX PT comprises testing an individual for homozygosity for a single
XX PT nucleotide polymorphism in the gene coding for the tumour necrosis
XX PT factor receptor II
XX
XX PS Disclosure: Page 7; 45pp; English.
XX
XX CC The present invention relates to a method for detecting non-responders
XX CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
XX CC an individual for homozygosity for at least one single nucleotide
XX CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
XX CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
XX CC A/G) and one in exon 6 (position 587 T/C) which result in Lys56Lys and
XX CC Met169Arg respectively, are also described. The method of the invention
XX CC is useful for detecting non-responders to anti-TNF therapy such as
XX CC infliximab therapy, or therapy of Crohn's disease. The genes containing
XX CC the 2 novel polymorphisms are useful for diagnostic purposes in
XX CC inflammatory, malignant or other chronic diseases. The present sequence
XX CC represents a TaqMan primer used in the methods of the present invention.
XX
XX SO Sequence 17 BP; 3 A; 8 C; 4 G; 2 T; 0 other:
XX
XX Query Match 67.8%; Score 12.2; DB 24; length 17;
XX Best Local Similarity 82.4%; Pred. No. 9.2e+03;
XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0.
XX
XX QY 1 CCCGGAAGGCACTCTGG 17
XX | | | | | | | | | | | | |
XX DB 17 CTCGGAGAAGCTGGCTGG 1
XX
XX RESULT 16
XX ID AAQ50876 standard; DNA: 20 BP.
XX
XX AC AAQ50876;
XX
XX DT 13-MAY-1994 (first entry)
XX
XX DE HSV2 primer.
XX
XX KW HSV; HSV2; herpes simplex virus; detection; body fluid; probe;
XX KW blotting; ss.
XX
XX OS Synthetic.
XX
XX PN JPO5260999-A.
XX
XX PD 12-OCT-1993.
XX
XX PF 16-MAR-1992; 92JP-0090268.
XX
XX PR 16-MAR-1992; 92JP-0090268.
XX
XX PA (IATR ) IATRON LAB INC.
XX

```

DR WPJ: 1993-356464/45.

PT Specific detection of herpes simplex virus 2 - using combination

XX of two primers with sequences from specified sequences of DNA

PS Disclosure: Page 6; 8pp; Japanese.

CC The primers are used for the rapid and specific detection of

CC herpes simplex virus 2 (HSV2) in body fluids (e.g. blister,

XX pharyngeal secretion and cerebrospinal fluid).

XX Sequence 20 BP; 3 A; 7 C; 10 G; 0 U; 0 other;

SQ

Query Match

Best local similarity 67.8%; Score 12.2; DB 14; Length 20;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCGAGACGACTGTGG 17
| | | | | | | | | | |
DB 3 CGCGAAGCAGGCCGG 19

RESULT 17

ID AAA15699/c

XX AAA15699 standard; DNA: 20 BP.

AC AAA15699;

XX

XX 03-AUG-2000 (first entry)

DE PCR primer #5 used in cancer suppressor gene identification.

XX

XX Cancer suppressor gene; large intestine cancer; treatment; tumour;

KW chromosome 14q32; PCR primer; ss.

OS Synthetic.

XX

XX WO200018911-A1.

PN

XX 06-APR-2000.

PD

XX

XX 30-SEP-1998; 98WO-CN00208.

FE

XX

XX 30-SEP-1998; 98WO-CN00208.

FR

XX

XX (ZHEN/) ZHENG S.

PA

XX

XX Zheng S, Cao J, Cao W, Geng L, Zhang Y;

PX

XX WPJ: 2000-293150/25.

DK

XX

XX Cancer-suppressor gene-down-regulated in large intestine cancer,

PT located in human chromosome 14q32, useful for diagnosis and treatment

PT of tumours particularly large intestine cancer

XX

XX Example 3; Page 18; 42pp; Chinese.

PS

CC This sequence represents a PCR primer used in an example of the

CC invention. The invention relates to a cancer-suppressor gene, which is

CC down regulated in large intestine cancer. The gene is located on

CC chromosome 14q32. The invention also relates to a vector comprising the

CC gene, a host cell transformed by the vector, and a process comprising the

CC polypeptide and antibody are used in the expression product. The gene, encoded

CC cancers particularly large intestine cancer.

XX

XX Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 other;

SQ

Query Match

Best local similarity 67.8%; Score 12.2; DB 21; Length 20;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCGAGACGACTGTGG 17

CC genes that control normal tissue development, cellular function,
 CC cellular proliferation and functional differentiation. C/EBP alpha (also
 CC known as CEBPA) is primarily found in tissues involved in energy
 CC metabolism which have a capacity to metabolise lipids, cholesterol and
 CC other sterols. It is thought to be involved in the regulation of
 CC adipocyte and chondrogenic differentiation, and is also involved in
 CC follicular development and ovulation, steroid-induced cell cycle arrest
 CC in the liver, in controlling glucose transporter GLUT2 promoter activity,
 CC in the hormonal regulation of metabolism, and in granulocyte development.
 CC The oligonucleotides of the invention are useful for diagnosis,
 CC prevention and treatment of conditions associated with C/EBP expression,
 CC such as cancer, tumour formation, infection, or inflammation.

XX
 SQ Sequence 20 BP; 3 A; 8 C; 6 G; 3 T; 0 other;

Query Match 67.8%; Score 12.2; DB 24; Length 20;
 Best Local Similarity 82.4%; Pred. No. 9.2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCGGAGAGCAGCTGTG 17
 |||||
 DB 17 CCTGACGCGCAGGCTGG 1

RESULT 19

ID ABL53569 standard; DNA; 24 BP.

AC ABL53569;

DT 10-JUN-2002 (first entry)

DE Human calcitonin 15.18 PCR primer #1.

KW Calcitonin 15.18; human; foetal abnormality; autoimmune disease;
 KW tumour; ageing; immunomodulator; cytostatic; gene therapy; PCR;
 KW primer; ss.

OS Homo sapiens.

PN WO200220778-A1.

PD 14-MAR-2002.

PF 02-JUL-2001; 2001WO-CN01124.

PR 07-JUL-2000; 2000CN-0117059.

PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

DR WPI: 2002-269626/31.

PT Human calcitonin 15.18 and encoding polynucleotide, used in diagnosis
 PT and treatment of malignant tumors, hemopathy, human immunodeficiency
 PT virus infection, immunological diseases and inflammation -

PS Example 2; Page 11; 32pp; Chinese.

CC The present invention relates to human calcitonin 15.18 (see
 CC AB075631). The calcitonin protein and its coding sequence are
 CC useful for the diagnosis and treatment of foetal abnormality,
 CC autoimmune disease, tumours, and for the study of human ageing.
 CC The present sequence is a PCR primer, which was used in an example
 CC from the invention.

XX
 SQ Sequence 24 BP; 3 A; 7 C; 12 G; 2 T; 0 other;

Query Match 67.8%; Score 12.2; DB 24; Length 24;
 Best Local Similarity 82.4%; Pred. No. 9.3e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CCGAAGCAGCTGTGC 18
 |||||
 DB 6 CAGCAGCAGCAGCTGC 22

RESULT 20

ID AAV08917 standard; DNA; 26 BP.

AC AAV08917;

DT 26-FEB-1999 (first entry)

DE PCR primer for SIV gag gene.

KW PCR primer; SIV; gp120 gene; gag gene; chimeric virus; SIV-HIV virus;
 KW AIDS-associated symptom; HIV; env protein; ss.

OS Synthetic.

OS Simian immunodeficiency virus.

PN US5849994-A.

PD 15-DEC-1998.

PF 16-MAY-1995; 95US-0442010.

PR 16-MAY-1995; 95US-0442010.

PA (UNIV) UNIV KANSAS MEDICAL CENT.

PI Narayan O;

DR WPI: 1999-069838/06.

PT Chimeric SIV-HIV virus - for producing AIDS symptoms in macaque
 PT monkeys
 PS Example; Column 15; 13pp; English.

CC This sequence represents a PCR primer for the simian immunodeficiency
 CC virus (SIV) gag gene. The amplified sequence can be used in the
 CC chimeric virus of the invention. The chimeric virus is a chimeric SIV-HIV
 CC virus (SHIV) that infects macaque monkeys and causes them to develop
 CC AIDS-associated symptoms within 32 weeks, where the virus is generated by
 CC at least two passages of a SHIV containing DNA encoding HIV env protein
 CC through macaque bone marrow in vivo. The monkeys are useful as an animal
 CC model for HIV-1-induced disease.

XX
 SQ Sequence 26 BP; 8 A; 5 C; 11 G; 2 T; 0 other;

Query Match 67.8%; Score 12.2; DB 20; Length 26;
 Best Local Similarity 82.4%; Pred. No. 9.3e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCGGAGAGCAGCTGTG 17
 |||||
 DB 1 CCAGGAGAGAGGCTGG 17

RESULT 21

ID AA087560/C standard; DNA; 32 BP.

AC AA087560;

DT 04-JAN-1996 (first entry)

DE HTLVIII amplification primer XHOM.

KW Human immunodeficiency virus; asymmetric; hammerhead; ribozyme; helix I;
 KW helix II; helix III; loop 2; cleavage site; amplification; PCR; primer;
 KW motif; construct; pathogen; retrovirus infection; ss.

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```
XX OS Synthetic.
XX FT Key
XX FT misc_binding
XX FT /tag=14..32
XX FT /note="binds to HTLVIII sequence"
XX PN W09510608-A1.
XX PD 20-APR-1995.
XX PF 15-OCT-1993; 93WO-EP02853.
XX PR 15-OCT-1993; 93WO-EP02853.
XX PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM STIFTUN.
XX PA (FORT-) FORT FOUND RES & TECHNOLOGY HELIAS.
XX PI Homann M, Szakiel G, Tabler M;
XX DR WPI: 1995-161795/21.
XX FT Asymmetric hammerhead ribozyme(s) and constructs - having high
XX FT catalytic activity and improved specificity for inactivating target
XX FT RNA e.g. in unwanted endogenous genes or pathogens
XX PS Example 2; Fig 7; 72pp; English.
XX CC A primer used in conjunction with primer A86B (AA087556) to generate an
XX CC inactive asymmetric ribozyme which lacks a nucleotide at position 12 of
XX CC the catalytic domain. The ribozyme is used as a control at position 12 of
XX CC an amplified region provides the Helix III and part of the Helix II of the
XX CC generated ribozyme. This is an example of an asymmetric ribozyme construct
XX CC (AA087567) that encodes the asymmetric ribozyme sequence GUC in the target
XX CC asymmetric ribozyme cleaves the HTLVIII RNA sequence AA087566. The
XX CC pathogenic RNA e.g. in viral or retroviral infections such as HIV
XX CC infection.
XX SQ Sequence 32 BP; 6 A; 9 C; 10 G; 7 T; 0 other;
XX QY Query Match
XX QY Best Local Similarity 67.8%; Score 12.2; DB 16; Length 32;
XX QY Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX DB 2 CCGAAGCAGCTGTGGC 18
XX DB 25 CCTCAAGCAGCTGTGGC 9
XX RESULT 22
XX ID AA089758/c
XX AC AA089758 standard; DNA; 32 BP.
XX XX
XX DT 08-FEB-1996 (first entry)
XX DE Primer XHOM to amplify HTLV-III bases 5819-6382.
XX DE Hammerhead ribozyme; catalytic site; helix; asymmetric; specificity; HIV;
XX DE Prokaryote; eukaryote; fruit ripening gene; protective agent; fungus;
XX DE Virus; insect pathogen; transgenic plant; transformed organism; PCR;
XX DE Polymerase chain reaction; primer; amplification; ss.
XX OS Synthetic.
XX FT Key
XX FT misc_binding
XX FT Location/Qualifiers
XX FT 14..32
```

```
XX FT /tag=14..32
XX FT /note="binds to template DNA pAR6 (AA089755)"
XX PN W09510609-A1.
XX PD 20-APR-1995.
XX PF 14-OCT-1994; 94WO-EP03391.
XX PR 15-OCT-1993; 93WO-EP02853.
XX PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM STIFTUN.
XX PA (FORT-) FORT FOUND RES & TECHNOLOGY HELIAS.
XX PI Homann M, Szakiel G, Tabler M;
XX DR WPI: 1995-161796/21.
XX FT Asymmetric hammerhead ribozymes - and corresp. coding constructs,
XX FT useful for inactivation or suppression of target genes, e.g. in
XX FT pathogens or during fruit ripening
XX PS Example 2; Fig 7b; 83pp; English.
XX CC Primers AA089756-8 were used to amplify bases 5845-6049 of the human
XX CC T-cell lymphotropic virus type III (HTLV-III) in plasmid pAR6
XX CC (AA089755). The amplified fragment was used to replace the helix I
XX CC sequence of construct pBS29-R2195 (AA089745). This primer helix I
XX CC is a non-functional control. The wild type from the catalytic domain
XX CC and cleaves the ribozyme (alpha)-R2195 (AA089754), which targets
XX CC sequence (AA08962). The construct was used in the generation of a
XX CC asymmetric ribozyme. The catalytic site of a hammerhead ribozyme
XX CC and a shortened helix I sequence. The ribozymes can be altered e.g. they
XX CC asymmetric in that they contain serially deleted helix I sequences (see
XX CC AA089772-80 for other examples). By interchanging the helix I and III
XX CC sequences, the specificity of the ribozymes can be altered e.g. they can
XX CC be used to inactivate or suppress target RNAs in prokaryote or eukaryote
XX CC cells such as suppressing certain fruit ripening genes or as protective
XX CC agents against fungal, viral or insect pathogens in transgenic plants or
XX CC transformed organisms.
XX SQ Sequence 32 BP; 6 A; 9 C; 10 G; 7 T; 0 other;
XX QY Query Match
XX QY Best Local Similarity 67.8%; Score 12.2; DB 16; Length 32;
XX QY Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX DB 2 CCGAAGCAGCTGTGGC 18
XX DB 25 CCTCAAGCAGCTGTGGC 9
XX RESULT 23
XX ID AA211413
XX AC AA211413 standard; DNA; 33 BP.
XX XX
XX DT 26-OCT-1999 (first entry)
XX DE Oligo for mutating natural splice donor site within a packaging signal.
XX DE Retroviral vector; functional splice donor site; hybrid viral vector;
XX DE functional splice acceptor site; in vivo gene delivery; therapeutic;
XX DE lentiviral vector; modified hematopoietic stem cell; MHC; tumor; MLV;
XX OS Ischemia; hypoxia response element; HRE; hypoxia; PCR primer; ss.
XX OS Synthetic.
XX FT Key
XX FT W09515684-A2.
```

PD 01-APR-1999.
XX
XX 23-SEP-1998; 98WO-GB02885.
XX
XX 25-SEP-1997; 97GB-0020465.
PR 23-SEP-1997; 97GB-0020216.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX Bebbington C, Binley KM, Lewis C, Naylor S;
PI WPI, 1999-263482/22.
XX
XX New retroviral vectors, for, e.g. delivering nucleotide sequences to
PT solid tumor sites
XX
XX Example 6; Page 177; 288pp; English.
XX
XX The invention relates to a retroviral vector (RVV) comprising a
CC functional splice donor site (FSDS) and a functional splice acceptor site
CC (FSAS) where: (i) the FSDS and the FSAS flank a first nucleotide sequence
CC of interest (NOI); (ii) the FSDS is upstream of the FSAS; (iii) the RVV
CC is derived from a retroviral pro-vector; (iv) the retroviral pro-vector
CC comprises a first nucleotide sequence (NS) capable of yielding the FSDS
CC and a second NS capable of yielding the FSAS; and (v) the first NS is
CC downstream of the second NS, such that the RVV is formed as a result of
CC reverse transcription of the retroviral pro-vector. A hybrid viral vector
CC (VV) system for in vivo gene delivery, which system comprises a primary
CC VV which encodes a secondary VV, the primary vector capable of infecting
CC a first target cell and of expressing the secondary VV, which secondary
CC vector is capable of transducing a secondary target cell, where the
CC primary vector is obtainable from or is based on an adenoviral vector and
CC the secondary VV is obtainable from or is based on an RVV preferably a
CC lentiviral vector (LVV) is also provided. The systems can be used for
CC delivering NOIs to one or more target sites. The NOIs may encode
CC therapeutic or diagnostic agents. The methods are used particularly for
CC producing modified hematopoietic stem cells (MNSCs) to deliver NOIs to
CC sites such as solid tumours, which are characterised by ischemia, such as
CC hypoxia or low glucose concentration. The system permits the stable
CC expression of NOIs in targeted cells, e.g. rapidly dividing cells.
XX
SQ Sequence 33 BP; 10 A; 11 C; 9 G; 3 T; 0 other;
Query Match 67.8%; Score 12.2; DB 20; Length 33;
Best Local Similarity 82.4%; Pred. No. 9.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 CCGGAAGGCACTGTGGC 18
 |||||
DB 7 CCGGAGGCAAGCTGGC 23
RESULT 24
AAA74925
ID AAA74925 standard; DNA; 36 BP.
AC AAA74925;
XX
XX 02-JAN-2001 (first entry)
DT
XX Nucleotide sequence of a substrate nucleic acid.
DE
XX Nucleic acid labelling; signal domain; substrate; signal template; ss.
KM
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 31..36
FT /*tag= a
FT /note= "template hybridisation domain"
XX
XX WO200046232-A1.
XX

PD 10-AUG-2000.
XX
XX 04-FEB-2000; 2000WO-US02897.
XX
XX 05-FEB-1999; 99US-0118721.
PR
XX (INTE-) INTEGRATED DNA TECHNOLOGIES INC.
XX
XX Behlke MA, Devor EJ, James SA, Walder JA;
PI WPI, 2000-514944/46.
XX
XX Labeling nucleic acid for detecting target nucleic acids, comprises
PT hybridising first and second nucleic acids with DNA polymerase and
PT labelled nucleotide, to create single domain hybridisable with signal
PT template domain
XX
XX Example 3; Page 35; 70pp; English.
XX
XX The specification describes a method for labelling a nucleic acid
CC molecule. The method comprises hybridising a first nucleic acid to
CC a second nucleic acid, and extending the second nucleic acid with a
CC DNA polymerase in the presence of a labelled nucleotide, to create
CC a signal domain having a sequence which shows complementarity towards
CC and is hybridisable to a signal template domain of the first nucleic
CC acid, so that the second nucleic acid is labelled. The first nucleic
CC acid comprises a substrate hybridisation domain of 5-20 nucleotides
CC and a signal template domain of 5-100, from 3' to 5'. The second
CC nucleic acid comprises a template hybridisation domain of 5-20 which
CC is not detectably labelled, and complementary to and hybridisable
CC with the substrate hybridisation domain of the first nucleic acid,
CC and a target binding domain which is not detectably labelled. The
CC method is useful for labelling nucleic acids, so that a labelled complex
CC of nucleic acid useful as probe is formed. The present sequence
CC represents a substrate nucleic acid of the invention.
XX
SQ Sequence 36 BP; 8 A; 8 C; 17 G; 3 T; 0 other;
Query Match 67.8%; Score 12.2; DB 21; Length 36;
Best Local Similarity 82.4%; Pred. No. 9.5e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CCGGAGGCAAGCTGTGG 17
 |||||
DB 3 CCGGAGGCAAGCTGTGG 19
RESULT 25
AAA74926
ID AAA74926 standard; DNA; 36 BP.
AC AAA74926;
XX
XX 02-JAN-2001 (first entry)
DT
XX Nucleotide sequence of a substrate nucleic acid.
DE
XX Nucleic acid labelling; signal domain; substrate; signal template; ss.
KM
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /note= "labelled with 32P"
XX
XX WO200046232-A1.
XX
XX 10-AUG-2000.
PD
XX 04-FEB-2000; 2000WO-US02897.
PE
XX 05-FEB-1999; 99US-0118721.
PR

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XX PA (INTE-) INTEGRATED DNA TECHNOLOGIES INC.
XX PI Behlke MA, Devor EJ, James SA, Walder JA;
XX WPI; 2000-514944/46.
XX
PT Labeling nucleic acid for detecting target nucleic acids, comprises
PT hybridising first and second nucleic acids with DNA polymerase and
PT labelled nucleotide, to create single domain hybridisable with signal
PT template domain
XX
PS Example 4; Page 39; 70pp; English.
XX
CC The specification describes a method for labelling a nucleic acid
CC molecule. The method comprises hybridising a first nucleic acid to
CC a second nucleic acid, and extending the second nucleic acid with a
CC DNA polymerase in the presence of a labelled nucleotide, to create
CC a signal domain having a sequence which shows complementarity towards
CC and is hybridisable to a signal template domain of the first nucleic
CC acid, so that the second nucleic acid is labelled. The first nucleic
CC acid comprises a substrate hybridisation domain of 3-20 nucleotides
CC and a signal template domain of 3-100, from 3' to 5'. The second
CC nucleic acid comprises a template hybridisation domain of 5-20 which
CC is not detectably labelled, and complementary to and hybridisable
CC with the substrate hybridisation domain of the first nucleic acid,
CC and a target binding domain which is not detectably labelled. The
CC method is useful for labelling nucleic acids, so that a labelled complex
CC of nucleic acid useful as probe is formed. The present sequence
CC represents a substrate nucleic acid of the invention.
XX
SQ Sequence 36 BP; 8 A; 8 C; 17 G; 3 T; 0 other;
XX
Query Match 67.8%; Score 12.2; DB 21; Length 36;
Best Local Similarity 82.4%; Pred. No. 9.5e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCGAGAGCGAGCTCG 17
Db 3 CCAGGAGAGGAGCGCTGG 19
XX
RESULT 26
AAAT4927
ID AAAT4927 standard; DNA; 46 BP.
XX
AC AAAT4927;
XX
DT 02-JAN-2001 (first entry)
XX
DE Nucleotide sequence of a substrate nucleic acid.
XX
KM Nucleic acid labelling; signal domain; substrate; signal template; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /note= "labelled with 32P"
XX
PN WO200046232-A1.
XX
PD 10-AUG-2000.
XX
PE 04-FEB-2000; 2000WO-US02897.
XX
PR 05-FEB-1999; 99US-0118721.
XX
PA (INTE-) INTEGRATED DNA TECHNOLOGIES INC.
XX
PI Behlke MA, Devor EJ, James SA, Walder JA;
XX

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DR WPI; 2000-514944/46.
XX
PT Labeling nucleic acid for detecting target nucleic acids, comprises
PT hybridising first and second nucleic acids with DNA polymerase and
PT labelled nucleotide, to create single domain hybridisable with signal
PT template domain
XX
PS Example 4; Page 39; 70pp; English.
XX
CC The specification describes a method for labelling a nucleic acid
CC molecule. The method comprises hybridising a first nucleic acid to
CC a second nucleic acid, and extending the second nucleic acid with a
CC DNA polymerase in the presence of a labelled nucleotide, to create
CC a signal domain having a sequence which shows complementarity towards
CC and is hybridisable to a signal template domain of the first nucleic
CC acid, so that the second nucleic acid is labelled. The first nucleic
CC acid comprises a substrate hybridisation domain of 3-20 nucleotides
CC and a signal template domain of 3-100, from 3' to 5'. The second
CC nucleic acid comprises a template hybridisation domain of 5-20 which
CC is not detectably labelled, and complementary to and hybridisable
CC with the substrate hybridisation domain of the first nucleic acid,
CC and a target binding domain which is not detectably labelled. The
CC method is useful for labelling nucleic acids, so that a labelled complex
CC of nucleic acid useful as probe is formed. The present sequence
CC represents a substrate nucleic acid of the invention.
XX
SQ Sequence 46 BP; 18 A; 8 C; 17 G; 3 T; 0 other;
XX
Query Match 67.8%; Score 12.2; DB 21; Length 46;
Best Local Similarity 82.4%; Pred. No. 9.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCGAGAGCGAGCTCG 17
Db 3 CCAGGAGAGGAGCGCTGG 19
XX
RESULT 27
AAL27830
ID AAL27830 standard; DNA; 50 BP.
XX
AC AAL27830;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #1038.
XX
KM Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KM neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
KM amyloid protein; angiotensin; apoptosis related protein; cadherin;
KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KM complement related protein; cytochrome; kinase; cytokine; interferon;
KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
KM multifactorial disease; autoimmune disease; infection;
KM nervous system disease; ss.
XX
OS Homo sapiens.
XX
FH Homo sapiens.
FT modified_base 1 /*tag= a
FT /note= "labelled with 32P"
XX
PN WO200047944-A2.
XX
PD 05-JUL-2001.
XX
PE 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
XX
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinketsu RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX

```

PT	Polyomorph nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT	oncogenes and histones, useful for diagnosing and treating, e.g.
PT	cancer, autoimmune diseases and infections -
PS	Claim 1; Page 1676; 4143pp; English.
XX	
CC	The present invention relates to oligonucleotides encoding polymorphic
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC	histones, kinases, colony stimulating factors, complement related
CC	proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC	G-protein coupled receptors and thioesterases. The present sequence is
CC	one such oligonucleotide. The oligonucleotides and the peptides encoded
CC	by them may be used in the prevention, diagnosis and treatment of
CC	diseases associated with inappropriate expression of the proteins listed
CC	above. Disorders that may be prevented, diagnosed and/or treated include
CC	multifactorial diseases with a genetic component, such as autoimmune
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,
CC	leukaemia), diseases of the nervous system and an infection of pathogenic
CC	organisms.
CC	
XX	
SO	Sequence 50 BP; 9 A; 10 C; 21 G; 10 T; 0 other;
	Query Match 67.8%; Score 12.2; DB 22; Length 50;
	Best Local Similarity 82.4%; Pred. No. 9.6e+03;
	Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0
OY	2 CCGAAGGCAGCTGGC 18
Db	4 CAGGAAGAGGCTGTGC 20
RESULT 28	
ID	AAS08378
XX	AAS08378 standard; DNA; 50 BP.
XX	
AC	AAS08378;
XX	
DT	23-OCT-2001 (first entry)
XX	
DE	Pig PHGPX 3' UTR oligonucleotide #4.
KW	Pig; phospholipid hydroperoxide glutathione peroxidase; PHGPX;
KW	Citrus stress-associated protein; Cit-SAP; antioxidant cosmetic;
KW	peroxidation; skin ageing; necrosis; skin lightening supporting agent;
XX	oligonucleotide; ss.
XX	
OS	Sus scrofa.
XX	
PN	EP111055-A1.
XX	
PD	27-JUN-2001.
XX	
PF	08-DEC-1999; 99EP-0403079.
XX	
PR	08-DEC-1999; 99EP-0403079.
XX	
PA	(VEIT-) VEITIGEN.
XX	
PI	Strosberg AD, Eshdat Y;
XX	
DR	WPI; 2001-419936/45.
XX	
XX	
PT	New phospholipid hydroperoxide glutathione peroxidase, useful for
PT	manufacturing antioxidant cosmetic for preventing lipid and
PT	phospholipid modification due to peroxidation, leading to damage of
PT	skin cells, ageing or necrosis -
XX	
PS	Example 6; Page 38; 61pp; English.
XX	
CC	The sequence represents an oligonucleotide used to construct the 3'

CC	UTR of pig PHGPx. The pig 3' UTR is added to a cDNA encoding orange
CC	phospholipid hydroperoxide glutathione peroxidase (PHGPx) (Citrus
CC	stress-associated protein, Ctl-SAP) mucelin, for expression in
CC	eukaryotic cells. The mutein has the cysteine at position 41 in the
CC	wild-type mutated to a selenocysteine, in order that the activity of the
CC	plant enzyme will be increased to resemble that of animal PHGPx enzymes.
CC	The plant PHGPx, its analogues, and plant enzymes having PHGPx activity
CC	are useful for manufacturing an antioxidant cosmetic or pharmaceutical
CC	dematological composition for preventing lipid and phospholipid
CC	modification due to their peroxidation, which may lead to damage of skin
CC	cells, ageing and/or necrosis. These may also be used to protect
CC	cells, lipids used in cosmetic compositions against phospholipid
CC	oxidation, and as skin-lightening supporting agents.
XX	
SQ	Sequence 50 BP; 11 A; 10 C; 12 G; 17 T; 0 other;
	Query Match 67.8% Score 12.2; DB 22; Length 50;
	Best Local Similarity 82.4% Pred. No. 9.6e+03;
	Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DG	1 CCCGGAGGCAGCTGG 17 30 CCCACAAAGCAGCCTGG 46
RESULT 29	
ID	ABA97719/c
AB	ABA97719 standard; DNA: 22 BP.
AC	
XX	ABA97719;
XX	
DT	18-JUN-2002 (first entry)
DE	
XX	Wolfram Syndrome 1 gene vector screening primer.
KW	Wolfram Syndrome 1, WFS1; transgenic; wolframin; brain; depression;
KM	stress-induced neurochemical change; behavioural change; mouse;
XX	drug screening; antidepressant; primer; ss.
OS	
PN	Unidentified.
PX	
XX	WO200191548-A2.
PD	
XX	06-DEC-2001.
PF	
XX	31-MAY-2001; 2001WO-US17652.
PR	
XX	01-JUN-2000; 2000US-209394P.
PA	(FHAA) PHARMACIA & UPJOHN CO.
XX	
PI	Roberds SL, Huff RM;
PT	
DR	WPI; 2002-089969/12.
XX	
PT	New transgenic non-human animals (mice), useful as models for
PT	depression, for monitoring the efficacy of a drug against depression,
PT	and for screening antidepressants, drugs or genes for ameliorating or
PT	treating depression -
PS	
XX	
XX	Example 1; Page 47; 65pp; English.
CC	
CC	The present sequence represents a screening primer, designated MF-FSC1,
CC	used to screen for homologous recombinants based on the Wolfram Syndrome
CC	1 (WFS1) gene vector sequence of the invention. The specification
CC	describes a non-human transgenic mammal comprising a genome containing a
CC	single copy of a wild-type WFS1 gene (see ABA97708) and a modified WFS1
CC	allele containing a mutation that disrupts the function of wolframin, or
CC	its transgenic progeny. Wolframin is a predicted transmembrane protein
CC	expressed in many tissues including pancreas and brain. The transgenic
CC	nonhuman animals are useful as models for depression, particularly as
CC	models for depression in humans. The animals exhibit chronic
CC	stress-induced neurochemical and behavioural changes associated with
CC	depression.

CC depression. The transgenic animals are also useful for screening or
 CC identifying antidepressant agents, drugs or genes that may be employed to
 CC alleviate or treat depression. The animals are also useful for
 CC monitoring the efficacy of a drug against depression.

XX Sequence 22 BP; 3 A; 8 C; 6 G; 5 T; 0 other;

Query Match 66.7%; Score 12; DB 24; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.2e+04; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGCAGCTCTGG 17
 DB 21 AAGCAGCTCTGG 10

RESULT 30
 AAV41645/C
 ID AAV41645 standard; DNA; 23 BP.

XX AAV41645;

XX 12-OCT-1998 (first entry)

XX Nucleotide sequence of PCR primer Neo-134R.

XX PCR; primer: amplification; transgenic animal; H2-M gene; cancer;
 XX inflammatory disease; graft rejection; autoimmune disease; ss.

XX Synthetic.

XX Mus sp.

XX BP853122-A2.

XX 15-JUL-1998.

XX 09-JAN-1998; 98BP-0300149.

XX 10-JAN-1997; 97US-0780949.

XX (ORTH) ORTHO PHARM CORP.

XX Karlsson L, Leung W, Peterson PA, Zhou L;

XX WPI; 1998-364648/32.

XX New transgenic animals which lack functional H2-M gene - used to
 XX develop agents for treating e.g. inflammation, graft rejection,
 XX autoimmune disease or cancer

XX Example 3; Page 8; 21pp; English.

XX This is the nucleotide sequence of a PCR primer used for amplification
 CC in the method of the invention involving novel transgenic animals
 CC lacking functional the H2-M gene. The transgenic animals can be used
 CC to establish a non-human model for diseases involving H2-M equivalents
 CC such as HLA-DM in humans. They can be used to identify agents for use
 CC in the treatment of e.g. inflammatory disease, graft rejection,
 CC autoimmune diseases or cancer.

XX Sequence 23 BP; 5 A; 8 C; 5 G; 5 T; 0 other;

Query Match 66.7%; Score 12; DB 19; Length 23;

Best Local Similarity 100.0%; Pred. No. 1.2e+04; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGCAGCTCTGG 17
 DB 23 AAGCAGCTCTGG 12

RESULT 31
 ABQ03907/C

ID ABQ03907 standard; DNA; 24 BP.

XX ABQ03907;

XX 11-JUN-2002 (first entry)

XX Oligonucleotide adapter/capture probe 3898.

XX Oligonucleotide array; adapter sequence; probe; ss.

XX Synthetic.

XX WO200216649-A2.

XX 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US26519.

XX 25-AUG-2000; 2000US-227948P.

XX 29-AUG-2000; 2000US-228854P.

XX (ILLU-) ILLUMINA INC.

XX Gunderson K;

XX WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting
 XX a target nucleic acid sequence, has different addresses comprising
 XX different specific capture probes

XX Claim 1; Page 136; 261pp; English.

XX The invention relates to an oligonucleotide array (1) comprising at least
 CC 25 different addresses (adapter sequences) with each comprising a
 CC different capture probe selected from a group consisting of the sequences
 CC given in ABQ00010-ABQ13409. (1) is useful for immobilising a target
 CC nucleic acid sequence by attaching a adapter nucleic acid
 CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
 CC nucleic acid and contacting the modified target nucleic acid with (1).
 CC The steps of above method is useful for detecting a target nucleic acid,
 CC which further comprises detecting the presence of the modified target
 CC nucleic acid.

XX Sequence 24 BP; 5 A; 7 C; 5 G; 7 T; 0 other;

Query Match 66.7%; Score 12; DB 24; Length 24;

Best Local Similarity 100.0%; Pred. No. 1.2e+04; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGAAGCAGCTC 14
 DB 19 CGAAGCAGCTC 8

RESULT 32
 AAX00963/C
 ID AAX00963 standard; DNA; 26 BP.

XX AAX00963;

XX 25-MAR-1999 (first entry)

XX ADA knock-out specific primer pck.

XX Adenosine; neuronal activity; pain syndrome; epilepsy; immortalised;
 XX ADA gene; acute trauma; osteoarthritis; burn; rheumatoid arthritis;
 XX knock-out; PCR primer; ss.

XX Synthetic.

XX Mus sp.

XX WO9858653-A1.

PD		30-DEC-1998.	
XX	PE	23-JUN-1996;	96WO-IB00973.
XX	PR	23-JUN-1997;	97US-0881038.
XX	PA	(BOIS/) BOISON D. (MOHL/) MOHLER H.	
XX	P1	Bolson D., Mohler H.; WPI; 1999-081040/07.	
DR	PT	Use of adenosine to inhibit neuronal activity in patient - by delivering chronic local dose to a site of activity to inhibit pain syndrome or epilepsy	
PS	SP	Examples; Page 22; 43pp; English.	
XX	CC	The invention relates to the use of adenosine for inhibiting neuronal activity in a patient having pain syndrome or epilepsy. A chronic local dose of adenosine delivered to a site of neuronal activity, inhibits the neuronal activity at the site and inhibits the pain syndrome or epilepsy. Methods of generating a conditionally immortalised adenosine-releasing cells are also provided. One method comprises generating a non-human animal embryo having an ADA gene (+/-) tsA58 (+/-) genotype and isolating conditionally immortalised adenosine-releasing cells from the embryo. The products and methods can be used for treating epilepsy or pain syndromes, e.g. pain associated with soft tissue disease and peripheral damage (e.g. acute trauma, osteoarthritis, rheumatoid arthritis, burns, epistomy), spinal pain, musculo-skeletal pain, upper-extremity pain, myofascial pain syndromes, headache, deep and visceral pain syndromes, (e.g. heart pain, muscle pain, eye pain, oculo-facial pain, abdominal pain, gynecological pain and pain during labour), pain associated with nerve and root damage (e.g. peripheral nerve disorders or infections, amputation-induced pain, peripheral neuropathies, tic douloureux and atypical facial pain, arachnoiditis), carcinoma-induced pain (particularly that involving bone and soft tissue sarcoma and metastases), and central nervous system induced pain (such as central pain due to spinal cord or brain stem damage). The local delivery of adenosine exhibits therapeutic effects without involving side effects associated with systemic administration. Sequences AX009637-67 represent allele-specific PCR primers used for genotyping cell lines having ADA gene (+/-) tsA58 (+/-) genotype. The present sequence is a ADA knock-out specific primer specific for the PGK promoter of the neomycin gene cassette used for the knock-out allele.	
SX	SO	Sequence 26 BP; 7 A; 7 C; 7 G; 5 T; 0 other:	
		Query Match 66.7%; Score 12; DB 20; Length 26; Best Local Similarity 100.0%; Pred. No. 1.2e+04; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
YY		6 AAGCAGCTGG 17 	
DY		17 AAGCAGCTGG 6	
ID	AAAS01072/c		
XX	AC	AAS01072 standard; DNA; 26 BP.	
XX	AC	AAS01072;	
DT	DE	29-MAY-2001 (first entry)	
XX	DD	PKLR-Vn/VEGF 5' transgene PCR primer R51.	
KM	Mouse;	phosphoglycerate kinase 1 promoter; targeting construct;	
KM	transgenic animal;	reporter expression cassette; luciferase marker;	
KM	vitreoplectin; FoslB; galactin 3'; VEGF; VEGFR; Tie2;	Selectable marker;	
KM	neomycin phosphotransferase II; chloramphenicol acetyltransferase;		

KW	thymidine kinase; PCR primer; ss.
XX	
OS	Mus sp.
XX	
PN	WO200118225-A1.
XX	
PD	15-MAR-2001.
XX	
PF	16-DEC-1999; 99WO-US30078.
XX	
PR	03-SEP-1999; 99US-0152522.
XX	
PA	(XENO-) XENOGEN CORP.
XX	
PI	Zhang N;
XX	
DR	WPI; 2001-203085/20.
XX	
PT	Targeting constructs and methods of using them for creating transgenic
PT	animals -
XX	
PS	Example 4; Page 53; 96pp; English.
XX	
CC	The present sequence for PCR primer R51 is used with PCR primer F51
CC	(AAS01071) to amplify a 1799 bp DNA fragment from the 5' end of the
CC	transgene that is integrated into the vltroectin site through homologous
CC	DNA recombination. The pTKR-Vh/VEGF targeting vector is an example of
CC	novel targeting constructs and methods of using them for creating
CC	transgenic animals in which at least 1 single-copy, non-essential gene is
CC	linked with a reporter expression cassette (e.g. a luciferase gene
CC	linked to a promoter heterologous to the single-copy, non-essential
CC	gene). The single-copy, non-essential gene may be selected from
CC	vltroectin (Vh), fosB and galactin 3. The promoter element may be
CC	selected from VEGF, VEGFR and Tle2. The constructs may contain a
CC	selectable marker e.g. neomycin phosphotransferase II, chloramphenicol
CC	acetyltransferase and thymidine kinase. The constructs are useful for
CC	creating transgenic animals in which at least 1 single-copy,
CC	non-essential gene is replaced with a reporter expression cassette.
CC	Methods of using these animals are also described.
XX	
SQ	Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 other;
XX	
Query Match	66.7%; Score 12; DB 22; Length 26;
Best Local Similarity	100.0%; Pred. NO. 1.2e+04;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	6 AAGCAGCTCTGG 17
Db	12 AAGCAGCTCTGG 1
XX	
RESULT 34	
AAF32217/c	
ID	AAF32217 standard; DNA; 26 BP.
XX	
AC	AAF32217;
XX	
DT	12-APR-2001 (first entry)
XX	
DE	Mouse Musashi 1 PCR primer SEQ ID NO:4.
XX	
KW	Mouse; Musashi 1; mutant; hydrocephaly; ontogenesis; PCR primer; ss.
XX	
OS	Mus sp.
XX	
PN	WO200101767-A1.
XX	
XX	
PD	11-JAN-2001.
XX	
PF	04-JUL-2000; 2000WO-JP04449.
XX	
PR	05-JUL-1999; 99JP-0190796.
XX	

PA	(NISC) JAPAN SCI & TECHNOLOGY CORP.
XX	
PI	Sakakibara S, Noda T, Okano H;
XX	
DR	WPI: 2001-138031/14.
XX	
PT	Hydrocephaly model animals obtained through ontogenesis of totipotent
PT	cell carrying a functionally deficient Musashi 1 gene, are useful in
XX	diagnosis and development of drugs for hydrocephaly
XX	
PS	Example; Page 16; 19pp; Japanese.
XX	
CC	The present invention describes hydrocephaly model animals which are
CC	not human mammals obtained through ontogenesis of a totipotent cell
CC	carrying a functionally deficient Musashi 1 gene transferred into them
CC	and their offspring, which are characterised by having the Musashi 1
CC	mutation gene in somatic chromosomes. The model animals are useful in
CC	studying the cause, diagnosis and development of drugs for congenital
CC	and difficult-to-treat hydrocephaly. With such animals, specific drugs
CC	and surgical procedures for hydrocephaly treatment can be obtained.
CC	AAFC2214 to AAFC2217 represent PCR primers for Musashi 1 which are
XX	used in an example from the present invention.
XX	
Sequence	26 BP; 6 A; 8 C; 7 G; 5 T; 0 other;
Query Match	66.7%; Score 12; DB 22; Length 26;
Best Local Similarity	100.0%; Pred. NO. 1.2e+04;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	6 AAGCGAGTCTGG 17
DB	13 AAGCGAGTCTGG 2
RESULT 35	
AAFC2210/C	
ID	AAFC2210 standard; DNA; 28 BP.
XX	
AC	AAFC2210;
XX	
DT	21-MAY-2001 (first entry)
XX	
DE	PCR primer for PKG.
XX	
KW	Alpha-tocopherol transport protein; alpha-TTP; knockout animal; diabetes;
KW	alpha-TTP inhibitor; vitamin E deficiency; arteriosclerosis; mouse;
KW	oxidative stress; PCR primer; PKG; ss.
OS	Synthetic.
XX	
PN	WO200113716-A1.
XX	
PD	01-MAR-2001.
XX	
PF	24-AUG-2000; 2000WO-jP05666.
XX	
PR	24-AUG-1999; 99JP-0237003.
XX	
PA	(INOUE) INOUE K.
PA	(ARAI) ARAI H.
XX	
PI	Inoue K, Arai H, Arita M, Jishage K, Suzuki H;
XX	
DR	WPI: 2001-218381/22.
XX	
PT	alpha-tocopherol transport protein knock-out animal, useful as tool for
PT	clarifying onset mechanism of diseases based on oxidation stress e.g.
PT	import vitamin E deficiency, arteriosclerosis and diabetes, and in drug
XX	development
XX	
PS	Example 2; Page 10; 41pp; Japanese.
XX	
CC	This invention relates to an alpha-tocopherol transport protein

```

CC (alpha-TTP) knockout animal. The non-human mammal is useful as a tool
CC determining the onset mechanisms of diseases which are based on
CC oxidation stress, e.g. inborn vitamin E deficiency, arteriosclerosis and
CC diabetes. The present sequence represents a PCR primer specific for PKC
CC
XX
SQ Sequence 28 BP; 6 A; 9 C; 7 G; 6 T; 0 other;
Query Match
Best Local Similarity 66.7%; Score 12; DB 22; Length 28;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps
OY 6 AAGCAGCTCTGG 17
Db 27 AAGCAGCTCTGG 16
|||||
RESULT 36
ABT03702/C
ID ABT03702 standard; DNA; 28 BP.
XX
AC ABT03702;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human Neurogenin-3 gene PCR primer SEQ ID NO: 223.
XX
DE Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
KW transcription factor; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200240716-A2.
XX
PD 23-MAY-2002.
XX
PP 13-NOV-2001; 2001MO-US43461.
XX
PR 16-NOV-2000; 2000US-249508P.
XX
PA (CEMT-) CEMINES LLC.
XX
PI Palm K;
XX
PI WPI; 2002-537346/57.
XX
DR
XX
PR Determining the presence of neoplastic molecular markers, by
PR identifying the presence of markers in host test sample using array of
PR neoplastic molecular marker specific reagents and analyzing the array
XX of the reagents
XX
XX Example 1; Page 17; 41pp; English.
XX
CC The present invention relates to a method for determining the presence of
CC neoplastic molecular markers in a host, involving the use of neoplastic
CC molecular marker specific reagents to detect such markers and analyzing
CC the array of reagents, allowing the identification of the neoplastic
CC disease present. This can be used to determine the best treatment for
CC cancer, in particular neural cell, lung and prostate tumours. The
CC present sequence is a PCR primer useful for detecting the coding
CC sequences of markers of the invention.
XX
SQ Sequence 28 BP; 11 A; 7 C; 6 G; 4 T; 0 other;
Query Match
Best Local Similarity 66.7%; Score 12; DB 24; Length 28;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps
OY 7 AGGAGCTCTGG 18
Db 28 AGGAGCTCTGG 17
|||||
RESULT 37

```

AAZ65981/c
ID AAZ65981 standard; DNA: 47 BP.
AC AAZ65981;
XX
XX
11-SEP-2001 (first entry)
XX
XX Human map-related diallelic marker SEQ ID NO:328.
XX
XX Human genome; diallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT variation replace(24,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX W09954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB00822.
XX
XX 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI: 2000-013267/01.
DR
XX
XX Novel diallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
XX Claim 1; Page 300; 2745pp; English.
XX
XX AAZ65654 to AAZ65578 represent human diallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ65579 to AAZ77440 represent amplification
CC primers for the diallelic markers. The diallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
XX
XX Sequence 47 BP; 10 A; 15 C; 13 G; 9 T; 0 other;
SQ
Query Match 66.7%; Score 12; DB 21; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 7 AGGACGCTGGC 18
DB 30 AGGACGCTGGC 19

RESULT 38
AAAT76214/c
ID AAAT76214 standard; DNA: 15 BP.
XX

AC AAAT76214;
XX
XX 12-SEP-1997 (first entry)
XX
XX
XX Human IL4 receptor antisense oligonucleotide.
XX
XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; interleukin; ss.
XX
XX Synthetic.
XX
XX W09640162-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US09306.
XX
XX 07-JUN-1995; 95US-0474497.
PR
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Metzger WJ, Nyce JW;
XX
XX WPI: 1997-051871/05.
DR
XX
XX Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject
XX
XX Example 5; Page 30; 71pp; English.
XX
XX
XX A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide
CC specific for the human IL4 receptor. The method can be used to
CC treat airway diseases such as cystic fibrosis, asthma, chronic
CC obstructive pulmonary disease, bronchitis and other airway diseases
CC characterised by an inflammatory response. By eliminating adenosine from
CC the antisense ON, its liberation upon antisense degradation is
CC prevented, thereby preventing adenosine-induced bronchoconstriction in
CC patients with hyper-reactive airways.
XX
XX
XX Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 other;
SQ
Query Match 65.6%; Score 11.8; DB 18; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 GGAAGCAGCTGGC 18
DB 15 GGAAGCAGCCAGCGC 1

RESULT 39
AAAX54009/c
ID AAAX54009 standard; DNA: 15 BP.
XX
XX
XX AAAX54009;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human IL-4 receptor antisense oligonucleotide fragment.
DE
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;

KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US19419.
XX
PR 09-JUN-1998; 98US-0093972.
XX 17-SEP-1997; 97US-0059160.
XX (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction
PS Disclosure; Page 49; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (AAK52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the junction between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences AAK55272-74. These multiple target
CC oligonucleotides (specifically AAK55180-771) can be used for the
CC antisense treatment of diseases and conditions. Typical diseases and
CC conditions are those associated with impaired respiration and
CC inflammation, including lung diseases, pulmonary vasoconstriction,
CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impaired
CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC hepatic metastases, as well as all types of cancers which may metastasize
CC or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 other;

Query Match 65.6%; Score 11.8; DB 20; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGAAGCAGCTGCGC 18
DB 15 GGAAGCAGCAGCAGC 1

RESULT 40
AAFI9575/C
ID AAF19575 standard; DNA; 15 BP.
XX
XX AAF19575;
AC
XX
DT 14-MAR-2001 (first entry)
XX
XX
DE Human IL4 receptor polynucleotide fragment #1142.
XX
KW low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiallergic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW

KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX Homo sapiens.
OS
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX (NYCE-) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not
XX trigger adenosine receptors during metabolism, useful e.g. for treating
XX cancers and respiratory obstructions -
XX
XX Claim 14; Page 208; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (1) comprising them, in the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (1) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543, represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 other;

Query Match 65.6%; Score 11.8; DB 21; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGAAGCAGCTGCGC 18
DB 15 GGAAGCAGCAGCAGC 1

Search completed: December 2, 2002, 12:49:01
Job time : 269 secs

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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 12:43:38 / Search time 47 Seconds
(Without alignments)
117.451 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 ccggaagcagctctgc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 / Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued_Patents_NA:*

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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCITUS.COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	15	83.3	25	1	US-08-447-179-7	Sequence 7, Appl
C 2	12.8	71.1	18	1	US-08-363-240A-1088	Sequence 1088, Ap
C 3	12.8	71.1	18	1	US-08-363-240A-1184	Sequence 1084, Ap
C 4	12.4	68.9	18	1	US-08-363-240A-1087	Sequence 1087, Ap
C 5	12.4	68.9	18	1	US-08-363-240A-1183	Sequence 1183, Ap
C 6	12.4	68.9	26	4	US-09-243-335-22	Sequence 22, Appl
C 7	12.2	67.8	20	4	US-09-593-589-37	Sequence 37, Appl
C 8	12.2	67.8	26	2	US-08-442-010-12	Sequence 12, Appl
C 9	12.2	67.8	28	6	546668-50	Patent No. 546668
C 10	12	66.7	23	3	US-08-780-949-2	Sequence 2, Appl
C 11	12	66.7	26	3	US-08-681-038A-1	Sequence 1, Appl
C 12	11.8	65.6	21	1	US-08-231-930-34	Sequence 34, Appl
C 13	11.8	65.6	21	1	US-08-367-122-34	Sequence 34, Appl
C 14	11.8	65.6	23	4	US-09-632-098-7	Sequence 7, Appl
C 15	11.8	65.6	24	4	US-09-199-637A-178	Sequence 178, Appl
C 16	11.8	65.6	24	4	US-07-885-689A-22	Sequence 22, Appl
C 17	11.6	64.4	27	4	US-09-253-396A-113	Sequence 113, Appl
C 18	11.6	64.4	29	3	US-08-840-062-12	Sequence 12, Appl
C 19	11.4	63.3	21	2	US-09-732-199A-22	Sequence 22, Appl
C 20	11.4	63.3	21	2	US-08-370-724-6	Sequence 6, Appl
C 21	11.4	63.3	21	4	US-08-659-877-6	Sequence 6, Appl
C 22	11.4	63.3	28	1	US-08-328-314-7	Sequence 7, Appl
C 23	11.4	63.3	28	1	US-08-731-045-7	Sequence 7, Appl
C 24	11.4	63.3	38	1	US-08-385-191A-7	Sequence 7, Appl
C 25	11.4	63.3	38	4	US-08-472-402A-7	Sequence 7, Appl
C 26	11.2	62.2	20	3	US-09-418-640-57	Sequence 57, Appl
C 27	11.2	62.2	20	4	US-09-109-663-15	Sequence 15, Appl

28	11.2	62.2	25	4	US-09-173-914-34	Sequence 34, Appl
29	11.2	62.2	25	4	US-09-593-012-129	Sequence 129, Appl
30	11.2	62.2	25	4	US-09-593-012-147	Sequence 147, Appl
31	11.2	62.2	27	2	US-08-259-609-12	Sequence 12, Appl
32	11.2	62.2	27	2	US-09-263-944-12	Sequence 12, Appl
33	11.2	62.2	27	4	US-09-305-463-12	Sequence 7, Appl
34	11.2	62.2	28	1	US-08-446-660-7	Sequence 7, Appl
35	11.2	62.2	28	4	US-08-974-302-7	Sequence 11, Appl
36	11.2	62.2	29	2	US-08-216-280-11	Sequence 10, Appl
37	11.2	62.2	29	4	US-08-604-165-10	Sequence 10, Appl
38	11.2	62.2	29	4	US-08-734-054B-10	Sequence 10, Appl
39	11.2	62.2	32	4	US-08-974-549A-625	Sequence 625, Appl
40	11.2	62.2	32	4	US-09-560-367A-17	Sequence 17, Appl
41	11.2	62.2	36	1	US-08-464-136-54	Sequence 64, Appl
42	11.2	62.2	36	1	US-08-440-787A-25	Sequence 25, Appl
43	11.2	62.2	36	1	US-08-440-787A-36	Sequence 36, Appl
44	11.2	62.2	36	2	US-08-349-131-64	Sequence 64, Appl
45	11.2	62.2	36	3	US-08-470-287A-64	Sequence 64, Appl
46	11.2	62.2	36	4	US-08-367-685-25	Sequence 25, Appl
47	11.2	62.2	36	5	PCT-US91-07411-25	Sequence 25, Appl
48	11.2	62.2	36	5	PCT-US91-07411-26	Sequence 25, Appl
49	11.2	62.2	36	5	PCT-US91-07419-59	Sequence 59, Appl
50	11.2	62.2	42	1	US-08-137-117D-59	Sequence 59, Appl
51	11.2	62.2	42	1	US-08-436-717-59	Sequence 59, Appl
52	11.2	62.2	42	2	US-08-805-918-53	Sequence 21, Appl
53	11.2	62.2	42	2	US-08-811-028-21	Sequence 21, Appl
54	11.2	62.2	42	2	US-08-584-040-8002	Sequence 8002, Ap
55	11.2	62.2	17	4	US-08-584-040-8398	Sequence 8398, Ap
56	11.2	62.2	18	4	US-09-490-692-136	Sequence 136, Appl
57	11.2	62.2	20	6	5256770-17	Patent No. 5256770
58	11.2	62.2	27	6	546668-57	Patent No. 546668
59	11.2	62.2	27	6	546668-17	Patent No. 546668
60	11.2	62.2	28	6	546668-57	Patent No. 546668
61	11.2	62.2	38	1	US-08-373-124A-1215	Sequence 1215, Ap
62	11.2	62.2	38	1	US-08-435-628-1215	Sequence 1215, Ap
63	11.2	62.2	42	1	US-08-171-389-1	Sequence 1, Appl
64	11.2	62.2	42	1	US-08-123-936-1	Sequence 1, Appl
65	11.2	62.2	42	2	US-08-475-228A-1	Sequence 1, Appl
66	11.2	62.2	42	3	US-08-482-080A-1	Sequence 1, Appl
67	11.2	62.2	42	3	US-09-354-947-1	Sequence 1, Appl
68	11.2	62.2	42	5	PCR-US93-12388-1	Sequence 35, Appl
69	11.2	62.2	16	1	US-08-093-884-35	Sequence 35, Appl
70	10.8	60.0	16	1	US-08-093-884-36	Sequence 36, Appl
71	10.8	60.0	16	1	US-08-093-884-38	Sequence 38, Appl
72	10.8	60.0	16	1	US-08-093-884-39	Sequence 39, Appl
73	10.8	60.0	16	4	US-09-394-457C-3	Sequence 3, Appl
74	10.8	60.0	16	4	US-09-709-556A-3	Sequence 3, Appl
75	10.8	60.0	17	4	US-08-584-040-8029	Sequence 6029, Ap
76	10.8	60.0	17	4	US-08-584-040-8030	Sequence 6030, Ap
77	10.8	60.0	19	4	US-09-328-907-489	Sequence 489, Appl
78	10.8	60.0	19	4	US-09-218-207-489	Sequence 489, Appl
79	10.8	60.0	20	4	US-09-593-289-38	Sequence 38, Appl
80	10.8	60.0	20	4	US-09-593-289-38	Sequence 38, Appl
81	10.8	60.0	21	3	US-08-488-942A-71	Sequence 71, Appl
82	10.8	60.0	21	3	US-08-488-942A-71	Sequence 71, Appl
83	10.8	60.0	21	3	US-08-488-208A-71	Sequence 71, Appl
84	10.8	60.0	21	4	US-08-488-211A-71	Sequence 71, Appl
85	10.8	60.0	21	4	US-08-488-223A-71	Sequence 71, Appl
86	10.8	60.0	21	4	US-08-438-431A-71	Sequence 71, Appl
87	10.8	60.0	22	4	US-09-066-047-22	Sequence 22, Appl
88	10.8	60.0	22	4	US-08-519-197-8	Sequence 8, Appl
89	10.8	60.0	25	4	US-09-538-709-444	Sequence 244, Appl
90	10.8	60.0	26	1	US-07-982-712-32	Sequence 32, Appl
91	10.8	60.0	28	2	US-08-859-998-840	Sequence 840, Appl
92	10.8	60.0	28	4	US-09-225-928-840	Sequence 26, Appl
93	10.8	60.0	32	2	US-09-001-826A-11	Sequence 11, Appl
94	10.8	60.0	32	1	US-07-602-824A-11	Sequence 11, Appl
95	10.8	60.0	32	1	US-07-983-451-11	Sequence 2, Appl
96	10.8	60.0	32	1	US-08-261-577-2	Sequence 66, Appl
97	10.8	60.0	36	4	US-08-977-131-66	Sequence 93, Appl
98	10.8	60.0	36	3	US-08-677-566-33	Sequence 15, Appl
99	10.8	60.0	36	4	US-09-452-817-15	Sequence 66, Appl
100	10.8	60.0	40	4	US-09-306-998-66	Sequence 66, Appl

C 101	10.8	60.0	40	4	US-09-452-817-14	Sequence 14, App1	C 174	10.6	58.9	41	1	US-08-409-442a-65	Sequence 65, App1
C 102	10.8	60.0	41	2	US-08-448-418-29	Sequence 29, App1	C 175	10.6	58.9	41	2	US-08-469-609a-65	Sequence 65, App1
C 103	10.8	60.0	42	1	US-07-885-689a-9	Sequence 9, App11	C 176	10.6	58.9	41	3	US-09-143-190-65	Sequence 65, App1
C 104	10.8	60.0	47	4	US-09-338-907-249	Sequence 249, App	C 177	10.6	58.9	41	4	US-09-502-344-65	Sequence 65, App1
C 105	10.8	60.0	47	4	US-09-338-907-326	Sequence 326, App	C 178	10.6	58.9	42	1	US-08-105-483-525	Sequence 225, App
C 106	10.8	60.0	47	4	US-09-218-207-349	Sequence 249, App	C 179	10.6	58.9	42	1	US-08-709-209-225	Sequence 225, App
C 107	10.8	60.0	47	4	US-09-218-207-326	Sequence 326, App	C 180	10.6	58.9	42	1	US-08-458-101-225	Sequence 225, App
C 108	10.8	60.0	50	2	US-08-709-368-2	Sequence 2, App11	C 181	10.6	58.9	42	2	US-08-486-969-37	Sequence 37, App1
C 109	10.6	58.9	18	4	US-08-363-240a-1086	Sequence 1086, Ap	C 182	10.6	58.9	42	2	US-08-486-969-41	Sequence 41, App1
C 110	10.6	58.9	18	4	US-09-156-828b-29	Sequence 29, App1	C 183	10.6	58.9	42	2	US-08-850-049-96	Sequence 96, App1
C 111	10.6	58.9	19	4	US-08-063-167a-41	Sequence 41, App1	C 184	10.6	58.9	42	2	US-08-050-478-96	Sequence 96, App1
C 112	10.6	58.9	20	1	US-08-063-167a-41	Sequence 41, App1	C 185	10.6	58.9	42	4	US-09-414-117-96	Sequence 96, App1
C 113	10.6	58.9	20	1	US-08-007-997a-41	Sequence 41, App1	C 186	10.6	58.9	42	4	US-09-678-437-96	Sequence 96, App1
C 114	10.6	58.9	20	2	US-08-440-740a-41	Sequence 41, App1	C 187	10.6	58.9	43	3	US-08-833-985-43	Sequence 43, App1
C 115	10.6	58.9	20	2	US-08-344-155c-41	Sequence 41, App1	C 188	10.6	58.9	43	4	US-09-410-903-93	Sequence 24, App1
C 116	10.6	58.9	20	3	US-09-048-804-2	Sequence 2, App11	C 189	10.6	58.9	44	1	US-08-259-148a-28	Sequence 28, App1
C 117	10.6	58.9	20	3	US-08-574-396-40	Sequence 40, App1	C 190	10.6	58.9	44	2	US-07-875-941a-44	Sequence 44, App1
C 118	10.6	58.9	20	3	US-08-982-845b-41	Sequence 41, App1	C 191	10.6	58.9	45	1	US-08-086-428b-119	Sequence 119, App
C 119	10.6	58.9	20	3	US-08-866-340-55	Sequence 55, App1	C 192	10.6	58.9	45	2	US-08-468-570-119	Sequence 119, App
C 120	10.6	58.9	20	3	US-08-991-525b-41	Sequence 41, App1	C 193	10.6	58.9	45	2	US-08-468-570-119	Sequence 119, App
C 121	10.6	58.9	20	3	US-09-085-759-41	Sequence 41, App1	C 194	10.6	58.9	45	5	PCT-US95-10398-223	Sequence 223, App1
C 122	10.6	58.9	20	4	US-09-128-496-41	Sequence 41, App1	C 195	10.6	58.9	47	1	US-08-482-882-92	Sequence 92, App1
C 123	10.6	58.9	20	4	US-09-103-875-61	Sequence 61, App1	C 196	10.6	58.9	47	1	US-08-483-889-92	Sequence 92, App1
C 124	10.6	58.9	20	4	US-08-973-556b-61	Sequence 40, App1	C 197	10.6	58.9	47	1	US-08-487-113d-92	Sequence 92, App1
C 125	10.6	58.9	20	4	US-09-488-744a-63	Sequence 63, App1	C 198	10.6	58.9	47	2	US-08-473-503-92	Sequence 92, App1
C 126	10.6	58.9	20	4	US-09-009-450a-41	Sequence 41, App1	C 199	10.6	58.9	47	2	US-08-483-932-92	Sequence 92, App1
C 127	10.6	58.9	20	4	US-09-295-593-19	Sequence 19, App1	C 200	10.6	58.9	47	2	US-08-720-420a-92	Sequence 92, App1
C 128	10.6	58.9	20	5	PCT-US93-08101-41	Sequence 41, App1	C 201	10.6	58.9	47	3	US-08-714-017-92	Sequence 92, App1
C 129	10.6	58.9	21	1	US-08-137-701-8	Sequence 8, App11	C 202	10.6	58.9	47	3	US-08-475-660-92	Sequence 92, App1
C 130	10.6	58.9	21	2	US-08-860-289-1	Sequence 1, App11	C 203	10.6	58.9	47	4	US-09-641-638-870	Sequence 870, App
C 131	10.6	58.9	21	4	US-09-287-623-1	Sequence 1, App11	C 204	10.6	58.9	49	4	US-09-318-448-29	Sequence 29, App1
C 132	10.6	58.9	21	4	US-09-156-828b-22	Sequence 22, App1	C 205	10.4	57.8	15	1	US-08-311-486c-171	Sequence 171, App
C 133	10.6	58.9	22	3	US-08-477-934-27	Sequence 27, App1	C 206	10.4	57.8	15	2	US-08-292-620a-374	Sequence 374, App
C 134	10.6	58.9	22	4	US-07-986-776a-27	Sequence 27, App1	C 207	10.4	57.8	15	3	US-09-071-845-578	Sequence 374, App
C 135	10.6	58.9	23	3	US-08-463-903-36	Sequence 36, App1	C 208	10.4	57.8	18	1	US-08-358-111-16	Sequence 16, App1
C 136	10.6	58.9	23	4	US-07-935-695-36	Sequence 36, App1	C 209	10.4	57.8	18	1	US-08-311-486c-1081	Sequence 1081, App
C 137	10.6	58.9	24	1	US-08-241-372-7	Sequence 7, App11	C 210	10.4	57.8	18	2	US-08-117-952-397	Sequence 397, App
C 138	10.6	58.9	24	1	US-08-110-294a-1	Sequence 1, App11	C 211	10.4	57.8	18	3	US-09-090-947-16	Sequence 16, App1
C 139	10.6	58.9	24	2	US-08-389-926-1	Sequence 1, App11	C 212	10.4	57.8	19	4	US-09-091-952a-185	Sequence 185, App
C 140	10.6	58.9	24	5	PCT-US95-05420-7	Sequence 7, App11	C 213	10.4	57.8	20	1	US-08-480-784-9	Sequence 9, App11
C 141	10.6	58.9	25	4	US-09-341-007b-8	Sequence 8, App11	C 214	10.4	57.8	20	1	US-08-483-553-9	Sequence 9, App11
C 142	10.6	58.9	26	1	US-07-724-500b-8	Sequence 8, App11	C 215	10.4	57.8	20	1	US-08-487-002-9	Sequence 9, App11
C 143	10.6	58.9	26	2	US-08-855-998-1016	Sequence 1016, App	C 216	10.4	57.8	20	1	US-08-483-554b-9	Sequence 9, App11
C 144	10.6	58.9	26	3	US-08-974-899-12	Sequence 22, App1	C 217	10.4	57.8	20	1	US-08-488-011b-9	Sequence 9, App11
C 145	10.6	58.9	26	4	US-09-225-928-1016	Sequence 1016, App	C 218	10.4	57.8	20	2	US-08-117-952-617	Sequence 617, App
C 146	10.6	58.9	28	6	546668-49	Patent No. 546668	C 219	10.4	57.8	20	3	US-09-344-001-41	Sequence 41, App1
C 147	10.6	58.9	30	1	US-07-989-160-2	Sequence 2, App11	C 220	10.4	57.8	20	3	US-09-166-186-228	Sequence 228, App
C 148	10.6	58.9	30	1	US-08-448-736-2	Sequence 2, App11	C 221	10.4	57.8	20	4	US-08-850-727-9	Sequence 2, App11
C 149	10.6	58.9	30	1	US-08-452-779-2	Sequence 2, App11	C 222	10.4	57.8	20	4	US-09-313-932-228	Sequence 228, App
C 150	10.6	58.9	30	1	US-08-445-065-2	Sequence 2, App11	C 223	10.4	57.8	20	4	US-09-312-932-380	Sequence 380, App
C 151	10.6	58.9	30	3	US-08-980-160A-5	Sequence 5, App11	C 224	10.4	57.8	20	4	US-09-657-481a-8	Sequence 89, App1
C 152	10.6	58.9	30	3	US-08-959-524-2	Sequence 2, App11	C 225	10.4	57.8	20	4	US-09-593-711a-115	Sequence 115, App
C 153	10.6	58.9	33	2	US-08-595-043a-83	Sequence 83, App1	C 226	10.4	57.8	20	5	PCT-US95-10202-9	Sequence 9, App11
C 154	10.6	58.9	33	3	US-08-888-841b-48	Sequence 48, App1	C 227	10.4	57.8	20	5	PCT-US95-10203-9	Sequence 9, App11
C 155	10.6	58.9	34	1	US-08-435-350-35	Sequence 35, App1	C 228	10.4	57.8	20	5	PCT-US95-10220-9	Sequence 9, App11
C 156	10.6	58.9	34	2	US-08-861-459-24	Sequence 24, App1	C 229	10.4	57.8	21	4	US-08-853-980-22	Sequence 22, App1
C 157	10.6	58.9	37	1	US-08-428-370A-13	Sequence 13, App1	C 230	10.4	57.8	21	4	US-08-943-731-96	Sequence 46, App
C 158	10.6	58.9	37	2	US-08-600-764-13	Sequence 13, App1	C 231	10.4	57.8	22	1	US-07-977-284a-30	Sequence 30, App1
C 159	10.6	58.9	38	2	US-08-124-981a-21	Sequence 21, App1	C 232	10.4	57.8	22	2	US-08-256-468b-30	Sequence 30, App1
C 160	10.6	58.9	38	3	US-09-037-190-19	Sequence 19, App1	C 233	10.4	57.8	23	1	US-08-211-202-31	Sequence 31, App1
C 161	10.6	58.9	38	3	US-09-037-192-19	Sequence 19, App1	C 234	10.4	57.8	23	1	US-08-307-619-11	Sequence 11, App1
C 162	10.6	58.9	38	3	US-09-037-143-19	Sequence 19, App1	C 235	10.4	57.8	23	2	US-08-350-260a-57	Sequence 57, App1
C 163	10.6	58.9	38	4	US-09-049-691-19	Sequence 19, App1	C 236	10.4	57.8	23	3	US-07-850-770-11	Sequence 11, App1
C 164	10.6	58.9	38	4	US-08-260-174-19	Sequence 19, App1	C 237	10.4	57.8	23	3	US-09-050-783-11	Sequence 11, App1
C 165	10.6	58.9	38	4	US-09-338-128a-19	Sequence 19, App1	C 238	10.4	57.8	23	3	PCT-US93-01398-11	Sequence 11, App1
C 166	10.6	58.9	38	4	US-09-233-346-19	Sequence 19, App1	C 239	10.4	57.8	24	2	US-08-859-998-807	Sequence 807, App
C 167	10.6	58.9	38	5	US-09-037-192-19	Sequence 19, App1	C 240	10.4	57.8	24	4	US-09-225-928-807	Sequence 19, App1
C 168	10.6	58.9	38	5	PCT-US92-08258-11	Sequence 11, App1	C 241	10.4	57.8	25	4	US-09-078-199-19	Sequence 20, App1
C 169	10.6	58.9	40	1	US-07-612-673-16	Sequence 16, App1	C 242	10.4	57.8	25	4	US-09-078-199-20	Sequence 20, App1
C 170	10.6	58.9	40	1	US-08-539-666-17	Sequence 17, App1	C 243	10.4	57.8	25	4	US-09-369-971-19	Sequence 19, App1
C 171	10.6	58.9	41	1	US-07-931-473b-65	Sequence 65, App1	C 244	10.4	57.8	25	4	US-09-369-971-20	Sequence 20, App1
C 172	10.6	58.9	41	1	US-07-714-110c-65	Sequence 65, App1	C 245	10.4	57.8	36	1	US-08-363-240a-409	Sequence 409, App
C 173	10.6	58.9	41	1	US-08-412-110-65	Sequence 65, App1	C 246	10.4	57.8	36	1	US-08-363-240a-936	Sequence 936, App

247	10.4	57.8	36	2	US-08-292-620A-1279	Sequence 1279, Ap	C 320	10.2	56.7	33	4	US-09-304-186-64	Sequence 64, Appl
248	10.4	57.8	36	3	US-08-856-074A-10	Sequence 10, Appl	C 321	10.2	56.7	34	1	US-07-998-978-10	Sequence 10, Appl
249	10.4	57.8	36	3	US-09-071-845-1279	Sequence 1279, Ap	C 322	10.2	56.7	34	2	US-08-452-800A-10	Sequence 10, Appl
250	10.4	57.8	38	1	US-08-211-203-44	Sequence 44, Appl	C 323	10.2	56.7	34	3	US-08-858-003-15	Sequence 15, Appl
251	10.4	57.8	38	1	US-08-373-124A-1199	Sequence 1199, Ap	C 324	10.2	56.7	34	3	US-09-078-166-15	Sequence 15, Appl
252	10.4	57.8	38	1	US-08-373-124A-1199	Sequence 1199, Ap	C 325	10.2	56.7	34	3	US-08-997-463-15	Sequence 15, Appl
253	10.4	57.8	38	1	US-08-435-628-1199	Sequence 1199, Ap	C 326	10.2	56.7	34	5	PCT-US92-11353-10	Sequence 10, Appl
254	10.4	57.8	38	2	US-08-435-628-1199	Sequence 1219, Ap	C 327	10.2	56.7	36	3	US-08-991-426-9	Sequence 9, Appl
255	10.4	57.8	38	2	US-08-293-620A-2039	Sequence 2039, Ap	C 328	10.2	56.7	36	3	US-08-968-563-26	Sequence 26, Appl
256	10.4	57.8	38	3	US-09-071-845-2039	Sequence 2039, Ap	C 329	10.2	56.7	36	3	US-09-143-470-26	Sequence 26, Appl
257	10.4	57.8	40	2	US-08-767-979-9	Sequence 9, Appl	C 330	10.2	56.7	36	3	US-09-143-470-26	Sequence 26, Appl
258	10.4	57.8	40	2	US-09-295-026-9	Sequence 9, Appl	C 331	10.2	56.7	36	3	US-08-966-662A-56	Sequence 56, Appl
259	10.4	57.8	50	2	US-08-389-548B-29	Sequence 29, Appl	C 332	10.2	56.7	36	3	US-08-966-662A-56	Sequence 56, Appl
260	10.4	57.8	50	3	US-08-389-548B-30	Sequence 30, Appl	C 333	10.2	56.7	36	3	US-08-966-662A-56	Sequence 56, Appl
261	10.4	57.8	50	3	US-08-466-047B-29	Sequence 29, Appl	C 334	10.2	56.7	36	4	US-09-311-847A-14	Sequence 14, Appl
262	10.4	57.8	50	3	US-08-466-047B-30	Sequence 30, Appl	C 335	10.2	56.7	36	4	US-09-307-872A-14	Sequence 14, Appl
263	10.4	57.8	50	3	US-08-983-607-6	Sequence 6, Appl	C 336	10.2	56.7	36	4	US-09-570-778A-3	Sequence 3, Appl
264	10.4	57.8	50	3	US-08-983-607-6	Sequence 6, Appl	C 337	10.2	56.7	37	1	US-08-290-592E-15	Sequence 15, Appl
265	10.2	56.7	16	4	US-09-156-828B-23	Sequence 23, Appl	C 338	10.2	56.7	37	5	PCT-US95-10533-12	Sequence 12, Appl
266	10.2	56.7	17	4	US-09-156-828B-23	Sequence 23, Appl	C 339	10.2	56.7	37	5	PCT-US96-09448-15	Sequence 15, Appl
267	10.2	56.7	18	3	US-08-584-940-7245	Sequence 7245, Ap	C 340	10.2	56.7	40	4	US-09-476-226-27	Sequence 27, Appl
268	10.2	56.7	18	3	US-09-255-911-23	Sequence 23, Appl	C 341	10.2	56.7	41	4	US-08-962-281-23	Sequence 23, Appl
269	10.2	56.7	19	1	US-08-584-940-8297	Sequence 8297, Ap	C 342	10.2	56.7	41	4	US-07-885-281-23	Sequence 23, Appl
270	10.2	56.7	19	2	US-08-684-773-1	Sequence 1, Appl	C 343	10.2	56.7	44	1	US-08-344-695-3	Sequence 3, Appl
271	10.2	56.7	20	1	US-08-309-768-1	Sequence 1, Appl	C 344	10.2	56.7	44	1	US-08-288-405A-17	Sequence 17, Appl
272	10.2	56.7	20	1	US-08-063-167A-64	Sequence 64, Appl	C 345	10.2	56.7	45	1	US-08-605-785-782	Sequence 782, Ap
273	10.2	56.7	20	1	US-08-907-997A-64	Sequence 64, Appl	C 346	10.2	56.7	47	4	US-09-641-638-1286	Sequence 1286, Ap
274	10.2	56.7	20	1	US-08-389-067-15	Sequence 15, Appl	C 347	10.2	56.7	50	1	US-07-718-490-1	Sequence 1, Appl
275	10.2	56.7	20	2	US-08-440-740A-64	Sequence 64, Appl	C 348	10.2	56.7	14	2	US-08-765-176-3	Sequence 3, Appl
276	10.2	56.7	20	2	US-08-440-740A-64	Sequence 64, Appl	C 349	10.2	56.7	16	1	US-08-311-760A-344	Sequence 344, Ap
277	10.2	56.7	20	2	US-08-982-845B-64	Sequence 64, Appl	C 350	10.2	56.7	16	1	US-08-774-310-34	Sequence 34, Appl
278	10.2	56.7	20	3	US-08-982-845B-64	Sequence 64, Appl	C 351	10.2	56.7	19	2	US-09-357-072-31	Sequence 31, Appl
279	10.2	56.7	20	3	US-08-982-845B-64	Sequence 64, Appl	C 352	10.2	56.7	19	2	US-08-611-280-6	Sequence 6, Appl
280	10.2	56.7	20	3	US-09-085-755-64	Sequence 64, Appl	C 353	10.2	56.7	19	4	US-09-195-990-6	Sequence 6, Appl
281	10.2	56.7	20	4	US-09-088-461-95	Sequence 95, Appl	C 354	10.2	56.7	20	2	US-08-611-280-6	Sequence 6, Appl
282	10.2	56.7	20	4	US-08-974-549A-551	Sequence 551, App	C 355	10.2	56.7	20	2	US-08-611-280-6	Sequence 6, Appl
283	10.2	56.7	20	4	US-09-128-496-64	Sequence 64, Appl	C 356	10.2	56.7	20	2	US-08-611-280-6	Sequence 6, Appl
284	10.2	56.7	20	4	US-09-161-540-14	Sequence 14, Appl	C 357	10.2	56.7	20	2	US-08-611-280-6	Sequence 6, Appl
285	10.2	56.7	20	4	US-09-487-445-35	Sequence 35, Appl	C 358	10.2	56.7	20	2	US-08-611-280-6	Sequence 6, Appl
286	10.2	56.7	20	4	US-09-009-490A-64	Sequence 64, Appl	C 359	10.2	56.7	20	2	US-08-611-280-6	Sequence 6, Appl
287	10.2	56.7	20	4	US-09-578-324-1	Sequence 1, Appl	C 360	10.2	56.7	20	4	US-08-611-280-6	Sequence 6, Appl
288	10.2	56.7	20	4	US-09-167-109-205	Sequence 109, Appl	C 361	10.2	56.7	20	4	US-08-611-280-6	Sequence 6, Appl
289	10.2	56.7	20	4	US-09-658-679A-12	Sequence 12, Appl	C 362	10.2	56.7	20	4	US-08-611-280-6	Sequence 6, Appl
290	10.2	56.7	20	5	PCT-US93-08101-64	Sequence 64, Appl	C 363	10.2	56.7	20	4	US-08-611-280-6	Sequence 6, Appl
291	10.2	56.7	21	2	US-08-837-190C-20	Sequence 20, Appl	C 364	10.2	56.7	21	1	US-08-451-777A-8	Sequence 8, Appl
292	10.2	56.7	21	4	US-09-243-335-28	Sequence 28, Appl	C 365	10.2	56.7	21	2	US-08-451-777A-8	Sequence 8, Appl
293	10.2	56.7	22	1	US-08-344-960-9	Sequence 9, Appl	C 366	10.2	56.7	21	2	US-08-451-777A-8	Sequence 8, Appl
294	10.2	56.7	23	3	US-08-755-587-163	Sequence 163, App	C 367	10.2	56.7	21	2	US-08-451-777A-8	Sequence 8, Appl
295	10.2	56.7	24	4	US-08-271-880A-137	Sequence 137, App	C 368	10.2	56.7	23	2	PCT-US95-06743-8	Sequence 8, Appl
296	10.2	56.7	25	1	US-08-315-671-3	Sequence 15, Appl	C 369	10.2	56.7	23	2	US-08-859-998-655	Sequence 655, App
297	10.2	56.7	25	2	US-08-858-933-3	Sequence 3, Appl	C 370	10.2	56.7	24	1	US-08-240-547-11	Sequence 11, Appl
298	10.2	56.7	25	3	US-08-271-880A-137	Sequence 137, App	C 371	10.2	56.7	24	1	US-08-240-547-11	Sequence 11, Appl
299	10.2	56.7	25	3	US-09-444-408-137	Sequence 4, Appl	C 372	10.2	56.7	24	3	US-08-466-860-67	Sequence 67, Appl
300	10.2	56.7	25	4	US-09-449-215-137	Sequence 137, App	C 373	10.2	56.7	24	3	US-08-466-860-67	Sequence 67, Appl
301	10.2	56.7	25	4	US-09-168-406A-4	Sequence 4, Appl	C 374	10.2	56.7	24	3	US-08-513-974B-220	Sequence 220, App
302	10.2	56.7	27	2	US-08-418-085A-25	Sequence 25, Appl	C 375	10.2	56.7	24	4	US-08-973-068-42	Sequence 42, Appl
303	10.2	56.7	27	4	US-09-099-011A-25	Sequence 25, Appl	C 376	10.2	56.7	24	4	US-08-276-776-67	Sequence 67, Appl
304	10.2	56.7	27	4	US-09-443-335-20	Sequence 20, Appl	C 377	10.2	56.7	26	4	US-08-471-309-67	Sequence 67, Appl
305	10.2	56.7	28	2	US-08-743-637B-125	Sequence 125, Appl	C 378	10.2	56.7	26	4	US-08-869-276-19	Sequence 19, Appl
306	10.2	56.7	28	3	US-08-526-840B-125	Sequence 125, Appl	C 379	10.2	56.7	26	4	US-09-635-344-19	Sequence 19, Appl
307	10.2	56.7	28	3	US-08-968-563-39	Sequence 39, Appl	C 380	10.2	56.7	27	3	US-09-398-629-19	Sequence 19, Appl
308	10.2	56.7	28	3	US-08-968-563-39	Sequence 39, Appl	C 381	10.2	56.7	28	1	US-08-513-974B-14	Sequence 14, Appl
309	10.2	56.7	29	1	US-08-166-664-1	Sequence 1, Appl	C 382	10.2	56.7	28	2	US-08-954-470-8	Sequence 8, Appl
310	10.2	56.7	29	2	US-08-481-753-8	Sequence 8, Appl	C 383	10.2	56.7	28	3	US-09-129-855A-8	Sequence 8, Appl
311	10.2	56.7	29	5	PCT-US93-07068-8	Sequence 8, Appl	C 384	10.2	56.7	28	4	US-09-247-152A-8	Sequence 8, Appl
312	10.2	56.7	32	1	US-07-621-193A-8	Sequence 8, Appl	C 385	10.2	56.7	29	3	US-09-257-739-8	Sequence 8, Appl
313	10.2	56.7	32	1	US-08-948-489C-8	Sequence 8, Appl	C 386	10.2	56.7	29	3	US-08-927-919A-15	Sequence 15, Appl
314	10.2	56.7	32	2	US-08-948-489C-8	Sequence 8, Appl	C 387	10.2	56.7	30	1	US-08-320-912A-102	Sequence 102, Appl
315	10.2	56.7	32	2	US-08-948-489C-8	Sequence 8, Appl	C 388	10.2	56.7	30	1	US-08-438-568A-7	Sequence 7, Appl
316	10.2	56.7	33	1	US-08-010-039-62	Sequence 62, Appl	C 389	10.2	56.7	30	2	US-08-872-034-10	Sequence 10, Appl
317	10.2	56.7	33	1	US-08-010-039-62	Sequence 62, Appl	C 390	10.2	56.7	30	3	US-08-872-034-10	Sequence 10, Appl
318	10.2	56.7	33	1	US-08-446-716-64	Sequence 64, Appl	C 391	10.2	56.7	30	3	US-08-872-034-10	Sequence 10, Appl
319	10.2	56.7	33	4	US-08-427-369-34	Sequence 34, Appl	C 392	10.2	56.7	33	2	US-08-577-492-29	Sequence 29, Appl

C 393	10	55.6	33	4	US-09-079-630-29	Sequence 29, Appl	466	9.8	54.4	20	3	US-09-289-267-61	Sequence 61, Appl
C 394	10	55.6	34	2	US-08-762-428A-8	Sequence 8, Appl	467	9.8	54.4	20	3	US-08-765-889C-6	Sequence 6, Appl
C 395	10	55.6	36	2	US-08-889-909A-17	Sequence 17, Appl	468	9.8	54.4	20	4	US-09-513-729B-68	Sequence 68, Appl
C 396	10	55.6	36	4	US-09-156-163A-17	Sequence 17, Appl	469	9.8	54.4	20	4	US-08-843-417-4	Sequence 4, Appl
C 397	10	55.6	39	2	US-08-750-810-5	Sequence 5, Appl	470	9.8	54.4	20	4	US-09-240-639-24	Sequence 24, Appl
C 398	10	55.6	39	2	US-08-244-548-2	Sequence 2, Appl	471	9.8	54.4	20	4	US-09-387-341-226	Sequence 226, App
C 399	10	55.6	40	1	US-08-199-507B-14	Sequence 14, Appl	472	9.8	54.4	20	4	US-09-851-896-19	Sequence 19, Appl
C 400	10	55.6	40	1	US-08-441-828-14	Sequence 14, Appl	473	9.8	54.4	20	4	US-09-658-679A-11	Sequence 11, Appl
C 401	10	55.6	40	2	US-08-470-939-42	Sequence 42, Appl	474	9.8	54.4	20	5	PCT-US95-07855-6	Sequence 6, Appl
C 402	10	55.6	40	2	US-09-113-750A-57	Sequence 57, Appl	475	9.8	54.4	21	2	US-08-753-979A-35	Sequence 35, Appl
C 403	10	55.6	40	4	US-09-141-027-14	Sequence 14, Appl	476	9.8	54.4	21	2	US-08-781-650B-4	Sequence 4, Appl
C 404	10	55.6	40	4	US-09-141-027-16	Sequence 16, Appl	477	9.8	54.4	21	4	US-09-493-461-10	Sequence 10, Appl
C 405	10	55.6	40	4	US-09-141-027-18	Sequence 18, Appl	478	9.8	54.4	21	4	US-09-493-461-18	Sequence 18, Appl
C 406	10	55.6	40	5	PCT-US96-09452-42	Sequence 42, Appl	479	9.8	54.4	21	4	US-09-177-650-13	Sequence 13, Appl
C 407	10	55.6	41	4	US-09-564-805-182	Sequence 182, App	480	9.8	54.4	22	1	US-08-479-723A-87	Sequence 87, Appl
C 408	10	55.6	42	3	US-08-955-636-12	Sequence 12, Appl	481	9.8	54.4	22	4	US-09-068-860-2	Sequence 2, Appl
C 409	10	55.6	42	4	US-09-202-101-13	Sequence 13, Appl	482	9.8	54.4	22	4	US-09-068-860-41	Sequence 41, Appl
C 410	10	55.6	42	4	US-09-191-468-18	Sequence 18, Appl	483	9.8	54.4	22	4	US-09-068-805-6	Sequence 6, Appl
C 411	10	55.6	43	1	US-08-253-877C-34	Sequence 34, Appl	484	9.8	54.4	22	4	US-09-068-805-7	Sequence 7, Appl
C 412	10	55.6	43	2	US-08-452-164A-34	Sequence 34, Appl	485	9.8	54.4	22	4	US-09-068-805-11	Sequence 11, Appl
C 413	10	55.6	45	2	US-08-690-495-23	Sequence 23, Appl	486	9.8	54.4	23	1	US-08-479-723A-78	Sequence 78, Appl
C 414	10	55.6	45	2	US-08-690-494-23	Sequence 23, Appl	487	9.8	54.4	23	2	US-08-823-516-105	Sequence 105, App
C 415	10	55.6	45	5	PCT-US95-07671-23	Sequence 23, Appl	488	9.8	54.4	23	3	US-08-759-038-90	Sequence 90, Appl
C 416	10	55.6	48	1	US-08-105-483-95	Sequence 95, Appl	489	9.8	54.4	23	3	US-08-759-038-90	Sequence 90, Appl
C 417	10	55.6	48	1	US-08-196-538-5	Sequence 5, Appl	490	9.8	54.4	23	4	US-09-092-077-8	Sequence 48, Appl
C 418	10	55.6	48	1	US-08-709-209-95	Sequence 95, Appl	491	9.8	54.4	23	4	US-09-068-805-8	Sequence 8, Appl
C 419	10	55.6	48	1	US-08-458-101-95	Sequence 95, Appl	492	9.8	54.4	24	2	US-08-859-998-964	Sequence 964, App
C 420	10	55.6	48	2	US-08-558-269-20	Sequence 20, Appl	493	9.8	54.4	24	3	US-08-483-316-2	Sequence 2, Appl
C 421	10	55.6	48	4	US-09-410-882-20	Sequence 20, Appl	494	9.8	54.4	24	4	US-09-074-658-74	Sequence 74, Appl
C 422	10	55.6	50	1	US-08-384-708A-117	Sequence 117, App	495	9.8	54.4	24	4	US-08-506-286B-15	Sequence 15, Appl
C 423	10	55.6	50	4	US-08-687-421-117	Sequence 117, App	496	9.8	54.4	24	4	US-09-225-928-864	Sequence 964, App
C 424	10	55.6	50	4	US-07-936-483-6	Sequence 6, Appl	497	9.8	54.4	24	5	PCT-US95-12624-2	Sequence 2, Appl
C 425	10	55.6	50	4	US-08-472-240A-26	Sequence 26, Appl	498	9.8	54.4	25	4	US-09-315-794-30	Sequence 30, Appl
C 426	9.8	54.4	17	4	US-08-584-040-2349	Sequence 2349, Ap	499	9.8	54.4	25	4	US-09-389-341-10	Sequence 30, Appl
C 427	9.8	54.4	17	4	US-08-584-040-5803	Sequence 5803, Ap	500	9.8	54.4	25	4	US-09-318-552A-15	Sequence 15, Appl
C 428	9.8	54.4	17	4	US-08-584-040-6031	Sequence 6031, Ap	501	9.8	54.4	26	2	US-08-337-562A-77	Sequence 77, Appl
C 429	9.8	54.4	18	1	US-07-685-722A-2	Sequence 2, Appl	502	9.8	54.4	26	4	US-09-318-503-18	Sequence 18, Appl
C 430	9.8	54.4	18	1	US-08-053-867A-9	Sequence 9, Appl	503	9.8	54.4	26	4	US-09-293-170-35	Sequence 35, Appl
C 431	9.8	54.4	18	1	US-08-050-073-278	Sequence 278, App	504	9.8	54.4	27	1	US-08-758-306-310	Sequence 310, App
C 432	9.8	54.4	18	2	US-08-585-684B-2552	Sequence 2552, Ap	505	9.8	54.4	27	1	US-08-758-306-694	Sequence 894, App
C 433	9.8	54.4	18	2	US-08-585-684B-2553	Sequence 2553, Ap	506	9.8	54.4	27	1	US-08-758-306-1272	Sequence 1272, Ap
C 434	9.8	54.4	18	3	US-09-106-038A-16	Sequence 16, Appl	507	9.8	54.4	27	4	US-08-506-286B-39	Sequence 39, Appl
C 435	9.8	54.4	18	3	US-09-106-038A-17	Sequence 17, Appl	508	9.8	54.4	27	4	US-08-584-040-6301	Sequence 6301, Ap
C 436	9.8	54.4	18	3	US-09-255-911-2	Sequence 2, Appl	509	9.8	54.4	27	4	US-09-294-894-6	Sequence 6, Appl
C 437	9.8	54.4	18	3	US-08-972-799A-18	Sequence 18, Appl	510	9.8	54.4	27	6	US-08-666-493-26	Sequence 26, Appl
C 438	9.8	54.4	18	3	US-09-195-666A-31	Sequence 31, Appl	511	9.8	54.4	28	2	US-08-859-998-546	Sequence 546, App
C 439	9.8	54.4	18	3	US-09-195-666A-32	Sequence 32, Appl	512	9.8	54.4	28	2	US-09-225-928-864	Sequence 546, App
C 440	9.8	54.4	18	4	US-09-038-073-2552	Sequence 2552, Ap	513	9.8	54.4	28	4	US-09-301-374-8	Sequence 8, Appl
C 441	9.8	54.4	18	4	US-09-038-073-2553	Sequence 2553, Ap	514	9.8	54.4	28	4	US-08-170-588-2	Sequence 2, Appl
C 442	9.8	54.4	18	4	US-09-506-282-18	Sequence 18, Appl	515	9.8	54.4	30	1	US-08-623-195-15	Sequence 15, Appl
C 443	9.8	54.4	18	4	US-09-632-380A-30	Sequence 30, Appl	516	9.8	54.4	30	1	US-08-184-009-201	Sequence 201, App
C 444	9.8	54.4	18	4	US-09-630-706-32	Sequence 32, Appl	517	9.8	54.4	30	2	US-08-482-182-2	Sequence 2, Appl
C 445	9.8	54.4	18	4	US-08-584-040-6246	Sequence 6246, Ap	518	9.8	54.4	30	2	US-08-458-336-201	Sequence 201, App
C 446	9.8	54.4	18	4	US-09-635-705-31	Sequence 31, Appl	519	9.8	54.4	30	2	US-08-460-736-201	Sequence 201, App
C 447	9.8	54.4	18	4	US-09-635-705-32	Sequence 32, Appl	520	9.8	54.4	30	4	US-08-891-282A-60	Sequence 60, Appl
C 448	9.8	54.4	18	4	US-09-634-858A-31	Sequence 31, Appl	521	9.8	54.4	30	4	US-09-039-982A-49	Sequence 49, Appl
C 449	9.8	54.4	18	4	US-09-634-858A-32	Sequence 32, Appl	522	9.8	54.4	31	4	US-09-039-982A-49	Sequence 49, Appl
C 450	9.8	54.4	18	5	PCT-US95-03339-18	Sequence 18, Appl	523	9.8	54.4	31	4	US-08-679-645-269	Sequence 269, App
C 451	9.8	54.4	19	1	US-08-050-073-277	Sequence 277, App	524	9.8	54.4	31	4	US-09-194-285-41	Sequence 41, Appl
C 452	9.8	54.4	19	1	US-08-456-923-11	Sequence 11, Appl	525	9.8	54.4	31	4	US-09-042-482D-49	Sequence 49, Appl
C 453	9.8	54.4	19	1	US-08-376-362A-6	Sequence 6, Appl	526	9.8	54.4	31	4	US-08-913-612A-55	Sequence 55, Appl
C 454	9.8	54.4	19	1	US-08-690-734A-83	Sequence 83, Appl	527	9.8	54.4	31	4	US-08-835-728D-55	Sequence 55, Appl
C 455	9.8	54.4	19	2	US-08-742-185-83	Sequence 83, Appl	528	9.8	54.4	32	3	US-08-835-728D-55	Sequence 55, Appl
C 456	9.8	54.4	19	4	US-09-038-637-140	Sequence 140, App	529	9.8	54.4	32	3	US-08-835-728D-159	Sequence 159, App
C 457	9.8	54.4	19	4	US-08-478-316-93	Sequence 93, Appl	530	9.8	54.4	32	4	US-09-490-558-159	Sequence 159, App
C 458	9.8	54.4	19	4	US-08-874-569B-17	Sequence 17, Appl	531	9.8	54.4	32	4	US-08-891-292A-64	Sequence 64, Appl
C 459	9.8	54.4	19	4	US-09-457-708-19	Sequence 19, Appl	532	9.8	54.4	32	4	US-09-234-326-8	Sequence 8, Appl
C 460	9.8	54.4	19	4	US-09-019-793A-93	Sequence 93, Appl	533	9.8	54.4	33	1	US-08-438-639-57	Sequence 57, Appl
C 461	9.8	54.4	20	1	US-08-484-192-72	Sequence 72, Appl	534	9.8	54.4	33	1	US-07-813-338A-57	Sequence 57, Appl
C 462	9.8	54.4	20	1	US-08-484-192-129	Sequence 129, App	535	9.8	54.4	33	1	US-08-470-124-67	Sequence 67, Appl
C 463	9.8	54.4	20	2	US-08-651-692-6	Sequence 6, Appl	536	9.8	54.4	33	2	US-09-078-459-73	Sequence 73, Appl
C 464	9.8	54.4	20	2	US-08-940-250-19	Sequence 19, Appl	537	9.8	54.4	33	2	US-08-441-971-133	Sequence 133, App
C 465	9.8	54.4	20	3	US-09-011-821-4	Sequence 4, Appl	538	9.8	54.4	33	3		

539	9.8	54.4	33	4	US-08-321-653-133	Sequence 133, App	C 612	9.6	53.3	20	1	US-08-050-073-114	Sequence 114, App
540	9.8	54.4	33	4	US-08-442-144A-133	Sequence 133, App	C 613	9.6	53.3	20	1	US-08-331-990-38	Sequence 38, App
541	9.8	54.4	33	4	US-08-830-828A-14	Sequence 14, App	C 614	9.6	53.3	20	1	US-08-367-122-38	Sequence 38, App
542	9.8	54.4	33	4	US-08-441-920A-13	Sequence 13, App	C 615	9.6	53.3	20	1	US-08-117-952-50	Sequence 50, App
543	9.8	54.4	33	5	PCT-US94-10257A-94	Sequence 94, App	C 616	9.6	53.3	20	2	US-08-468-352-30	Sequence 30, App
544	9.8	54.4	34	4	US-09-167-985-14	Sequence 14, App	C 617	9.6	53.3	20	2	US-08-693-211-34	Sequence 34, App
545	9.8	54.4	36	1	US-07-721-958-1	Sequence 1, App	C 618	9.6	53.3	20	2	US-08-649-816-2	Sequence 2, App
546	9.8	54.4	36	1	US-07-834-539A-11	Sequence 11, App	C 619	9.6	53.3	20	3	US-08-517-256-7	Sequence 7, App
547	9.8	54.4	36	1	US-08-436-539A-11	Sequence 11, App	C 620	9.6	53.3	20	3	US-08-286-904-6	Sequence 6, App
548	9.8	54.4	36	1	US-08-053-604-3	Sequence 3, App	C 621	9.6	53.3	20	4	US-09-433-613-7	Sequence 7, App
549	9.8	54.4	36	1	US-08-203-387-3	Sequence 3, App	C 622	9.6	53.3	20	4	US-09-504-245-7	Sequence 7, App
550	9.8	54.4	36	1	US-07-853-408B-19	Sequence 19, App	C 623	9.6	53.3	20	4	US-09-287-682-7	Sequence 7, App
551	9.8	54.4	36	2	US-08-006-782-19	Sequence 19, App	C 624	9.6	53.3	20	4	US-09-287-679-7	Sequence 7, App
552	9.8	54.4	36	2	US-08-808-353-11	Sequence 11, App	C 625	9.6	53.3	20	4	US-09-397-766-7	Sequence 7, App
553	9.8	54.4	36	4	US-09-508-865-19	Sequence 19, App	C 626	9.6	53.3	20	4	US-09-287-681-7	Sequence 7, App
554	9.8	54.4	36	4	US-08-042-353-187	Sequence 187, App	C 627	9.6	53.3	20	4	US-09-662-249A-32	Sequence 32, App
555	9.8	54.4	36	5	PCT-US92-06185-11	Sequence 35, App	C 628	9.6	53.3	20	4	US-09-495-444-7	Sequence 7, App
556	9.8	54.4	36	5	PCT-US92-06185-11	Sequence 35, App	C 629	9.6	53.3	20	4	US-09-337-388-2	Sequence 7, App
557	9.8	54.4	37	1	US-08-255-670A-7	Sequence 19, App	C 630	9.6	53.3	20	4	US-09-742-703-20	Sequence 20, App
558	9.8	54.4	37	1	US-08-390-850-838	Sequence 838, App	C 631	9.6	53.3	20	4	US-09-702-327-14	Sequence 14, App
559	9.8	54.4	38	1	US-08-373-124A-1694	Sequence 838, App	C 632	9.6	53.3	20	4	US-09-923-871C-31	Sequence 31, App
560	9.8	54.4	38	1	US-08-435-634-838	Sequence 838, App	C 633	9.6	53.3	20	4	US-08-943-731-360	Sequence 360, App
561	9.8	54.4	38	2	US-08-435-628-1694	Sequence 1694, App	C 634	9.6	53.3	22	1	US-08-643-181-28	Sequence 28, App
562	9.8	54.4	38	2	US-08-292-620A-2271	Sequence 2271, App	C 635	9.6	53.3	24	2	US-08-559-998-1201	Sequence 1201, App
563	9.8	54.4	38	3	US-09-071-845-2271	Sequence 2271, App	C 636	9.6	53.3	24	2	US-08-559-998-1201	Sequence 1201, App
564	9.8	54.4	39	1	US-07-834-539A-48	Sequence 48, App	C 637	9.6	53.3	24	2	US-09-061-764A-23	Sequence 23, App
565	9.8	54.4	39	1	US-08-053-131-60	Sequence 60, App	C 638	9.6	53.3	24	2	US-09-225-928-1201	Sequence 23, App
566	9.8	54.4	39	1	US-08-645-64-60	Sequence 60, App	C 639	9.6	53.3	24	2	US-08-556-965-3	Sequence 3, App
567	9.8	54.4	39	1	US-08-096-762-60	Sequence 60, App	C 640	9.6	53.3	25	3	US-08-946-914-46	Sequence 46, App
568	9.8	54.4	39	2	US-08-414-657D-40	Sequence 40, App	C 641	9.6	53.3	25	3	US-08-946-914-53	Sequence 53, App
569	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 642	9.6	53.3	25	3	US-08-946-914-60	Sequence 60, App
570	9.8	54.4	39	2	US-08-308-865-60	Sequence 60, App	C 643	9.6	53.3	25	3	US-09-021-701-12	Sequence 12, App
571	9.8	54.4	39	2	US-08-732-708C-28	Sequence 28, App	C 644	9.6	53.3	25	4	US-09-021-701-13	Sequence 13, App
572	9.8	54.4	39	3	US-09-233-493-18	Sequence 18, App	C 645	9.6	53.3	25	4	US-09-021-701-14	Sequence 14, App
573	9.8	54.4	39	3	US-09-005-476-18	Sequence 18, App	C 646	9.6	53.3	25	4	US-09-021-701-15	Sequence 15, App
574	9.8	54.4	39	3	US-09-042-353-223	Sequence 223, App	C 647	9.6	53.3	25	4	US-09-021-701-16	Sequence 16, App
575	9.8	54.4	39	4	US-09-233-492-18	Sequence 18, App	C 648	9.6	53.3	25	4	US-09-021-701-17	Sequence 17, App
576	9.8	54.4	39	4	US-08-296-280-18	Sequence 18, App	C 649	9.6	53.3	25	4	US-09-021-701-18	Sequence 18, App
577	9.8	54.4	39	4	US-08-758-417A-71	Sequence 71, App	C 650	9.6	53.3	25	4	US-09-021-701-19	Sequence 19, App
578	9.8	54.4	39	5	US-09-135-080-28	Sequence 28, App	C 651	9.6	53.3	25	4	US-09-021-701-20	Sequence 20, App
579	9.8	54.4	39	5	PCT-US92-06185-48	Sequence 48, App	C 652	9.6	53.3	25	4	US-09-021-701-21	Sequence 21, App
580	9.8	54.4	39	5	PCT-US92-06185-48	Sequence 48, App	C 653	9.6	53.3	25	4	US-09-021-701-22	Sequence 22, App
581	9.8	54.4	39	5	PCT-US92-06185-48	Sequence 48, App	C 654	9.6	53.3	25	4	US-09-021-701-23	Sequence 23, App
582	9.8	54.4	40	1	US-08-066-961-34	Sequence 34, App	C 655	9.6	53.3	25	4	US-09-656-450-46	Sequence 46, App
583	9.8	54.4	40	2	US-08-336-198C-4	Sequence 34, App	C 656	9.6	53.3	25	4	US-09-656-450-53	Sequence 53, App
584	9.8	54.4	41	2	US-08-857-946-68	Sequence 68, App	C 657	9.6	53.3	25	4	US-09-656-450-60	Sequence 60, App
585	9.8	54.4	41	2	US-08-857-946-68	Sequence 68, App	C 658	9.6	53.3	27	2	US-08-432-693-9	Sequence 9, App
586	9.8	54.4	41	3	US-08-970-740-68	Sequence 68, App	C 659	9.6	53.3	27	2	US-09-283-396A-75	Sequence 75, App
587	9.8	54.4	42	1	US-08-338-992B-9	Sequence 9, App	C 660	9.6	53.3	28	1	US-07-640-748-3	Sequence 3, App
588	9.8	54.4	42	2	US-08-850-049-95	Sequence 95, App	C 661	9.6	53.3	29	1	US-08-649-619B-4	Sequence 4, App
589	9.8	54.4	42	2	US-08-050-478-95	Sequence 95, App	C 662	9.6	53.3	29	2	US-08-661-459-27	Sequence 27, App
590	9.8	54.4	42	2	US-09-114-117-95	Sequence 95, App	C 663	9.6	53.3	29	2	US-08-814-567A-23	Sequence 23, App
591	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 664	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
592	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 665	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
593	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 666	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
594	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 667	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
595	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 668	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
596	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 669	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
597	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 670	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
598	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 671	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
599	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 672	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
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602	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 675	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
603	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 676	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
604	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 677	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
605	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 678	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
606	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 679	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
607	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 680	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
608	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 681	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
609	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 682	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
610	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 683	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App
611	9.8	54.4	42	4	US-09-010-733-9	Sequence 9, App	C 684	9.6	53.3	30	1	US-08-814-572C-15	Sequence 15, App

665	9.6	53.3	35	4	US-09-352-654A-51	Sequence 51, Appl	C 758	9.6	53.3	50	2	US-08-635-761-26	Sequence 26, Appl
C 666	9.6	53.3	35	4	US-09-348-097-50	Sequence 50, Appl	C 759	9.6	53.3	50	2	US-08-635-761-27	Sequence 27, Appl
667	9.6	53.3	35	4	US-09-348-097-51	Sequence 51, Appl	C 760	9.6	53.3	50	2	US-08-635-761-28	Sequence 28, Appl
C 668	9.6	53.3	35	4	US-09-276-553A-8	Sequence 8, Appl	761	9.6	53.3	50	4	US-09-091-814-13	Sequence 13, Appl
669	9.6	53.3	36	4	US-09-250-580-3	Sequence 3, Appl	C 762	9.6	53.3	50	4	US-09-021-701-9	Sequence 9, Appl
680	9.6	53.3	37	1	US-08-591-452-17	Sequence 17, Appl	C 763	9.6	53.3	50	4	US-09-312-520-25	Sequence 25, Appl
C 681	9.6	53.3	37	3	US-08-938-830-57	Sequence 57, Appl	C 764	9.6	53.3	50	4	US-09-312-520-26	Sequence 26, Appl
C 682	9.6	53.3	37	3	US-08-858-003-13	Sequence 13, Appl	C 765	9.6	53.3	50	4	US-09-312-520-27	Sequence 27, Appl
C 683	9.6	53.3	37	3	US-09-078-166-13	Sequence 13, Appl	C 766	9.6	53.3	50	4	US-09-312-520-28	Sequence 28, Appl
C 684	9.6	53.3	37	4	US-08-997-467-13	Sequence 13, Appl	C 767	9.6	53.3	50	4	US-09-538-709-95	Sequence 95, Appl
685	9.6	53.3	38	1	US-08-106-078-5	Sequence 5, Appl	C 768	9.6	53.3	50	4	US-09-538-709-1262	Sequence 1262, Ap
C 686	9.6	53.3	38	1	US-08-591-452-5	Sequence 5, Appl	C 769	9.4	52.2	11	5	PCT-US94-05659-24	Sequence 24, Appl
697	9.6	53.3	38	2	US-08-276-967-4	Sequence 4, Appl	C 770	9.4	52.2	15	1	US-08-311-486C-172	Sequence 172, Ap
C 698	9.6	53.3	39	1	US-08-106-078-1	Sequence 1, Appl	C 771	9.4	52.2	15	2	US-08-292-620A-375	Sequence 375, Ap
699	9.6	53.3	39	1	US-08-631-200-6	Sequence 6, Appl	C 772	9.4	52.2	15	3	US-09-071-845-375	Sequence 375, Ap
C 700	9.6	53.3	39	1	US-08-591-492-1	Sequence 1, Appl	C 773	9.4	52.2	16	4	US-08-413-974-16	Sequence 16, Appl
701	9.6	53.3	39	1	US-08-829-553-6	Sequence 6, Appl	C 774	9.4	52.2	16	4	US-08-433-418-16	Sequence 16, Appl
C 702	9.6	53.3	39	2	US-08-922-267A-6	Sequence 6, Appl	C 775	9.4	52.2	16	4	US-08-433-288-16	Sequence 16, Appl
703	9.6	53.3	39	2	US-08-936-707A-6	Sequence 6, Appl	C 776	9.4	52.2	16	4	US-08-174-739A-16	Sequence 16, Appl
C 704	9.6	53.3	39	2	US-08-936-706A-6	Sequence 6, Appl	C 777	9.4	52.2	16	4	US-08-434-256-16	Sequence 16, Appl
705	9.6	53.3	39	3	US-09-248-203-6	Sequence 6, Appl	C 778	9.4	52.2	17	4	US-09-282-147-26	Sequence 26, Appl
C 706	9.6	53.3	39	3	US-09-091-348-14	Sequence 14, Appl	779	9.4	52.2	17	4	US-09-560-639-30	Sequence 30, Appl
C 707	9.6	53.3	39	4	US-09-406-071-6	Sequence 6, Appl	C 780	9.4	52.2	17	5	PCT-US91-03056-14	Sequence 14, Appl
C 708	9.6	53.3	40	2	US-08-596-387B-65	Sequence 65, Appl	C 781	9.4	52.2	18	1	US-08-647-584-12	Sequence 12, Appl
C 709	9.6	53.3	40	2	US-08-596-387B-66	Sequence 66, Appl	C 782	9.4	52.2	18	3	US-09-344-579-93	Sequence 43, Appl
C 710	9.6	53.3	40	4	US-09-067-615-65	Sequence 65, Appl	C 783	9.4	52.2	18	3	US-09-143-212-74	Sequence 74, Appl
711	9.6	53.3	40	4	US-09-067-615-66	Sequence 66, Appl	C 784	9.4	52.2	18	3	US-09-163-162-31	Sequence 31, Appl
C 712	9.6	53.3	40	5	PCT-US95-09816A-65	Sequence 65, Appl	C 785	9.4	52.2	18	4	US-09-266-407-31	Sequence 31, Appl
713	9.6	53.3	40	5	PCT-US95-09816A-66	Sequence 66, Appl	C 786	9.4	52.2	18	4	US-09-496-654B-40	Sequence 40, Appl
714	9.6	53.3	41	1	US-08-040-548-57	Sequence 57, Appl	C 787	9.4	52.2	18	4	US-09-496-654B-80	Sequence 80, Appl
715	9.6	53.3	41	1	US-08-466-344-57	Sequence 57, Appl	C 788	9.4	52.2	18	4	US-09-723-535-18	Sequence 18, Appl
C 716	9.6	53.3	41	2	US-08-781-620B-10	Sequence 10, Appl	C 789	9.4	52.2	19	1	US-08-605-089-11	Sequence 11, Appl
C 717	9.6	53.3	41	2	US-09-313-221A-28	Sequence 28, Appl	790	9.4	52.2	20	1	US-07-743-518-4	Sequence 4, Appl
718	9.6	53.3	42	1	US-08-137-117D-59	Sequence 59, Appl	791	9.4	52.2	20	1	US-07-743-518-9	Sequence 9, Appl
C 719	9.6	53.3	42	1	US-08-436-717-59	Sequence 59, Appl	792	9.4	52.2	20	1	US-07-977-284A-112	Sequence 112, Ap
C 720	9.6	53.3	43	1	US-08-578-669-15	Sequence 15, Appl	793	9.4	52.2	20	1	US-08-250-866A-33	Sequence 33, Appl
C 721	9.6	53.3	43	1	US-08-471-791-37	Sequence 37, Appl	794	9.4	52.2	20	1	US-08-271-880A-183	Sequence 183, Ap
722	9.6	53.3	44	4	US-09-142-334-14	Sequence 14, Appl	C 795	9.4	52.2	20	1	US-08-741-406-9	Sequence 9, Appl
C 723	9.6	53.3	44	5	PCT-US91-01746-37	Sequence 37, Appl	C 796	9.4	52.2	20	2	US-08-411-098-37	Sequence 37, Appl
C 724	9.6	53.3	45	1	US-07-946-421-36	Sequence 36, Appl	C 797	9.4	52.2	20	2	US-08-117-992-497	Sequence 497, Ap
725	9.6	53.3	45	1	US-08-459-310-6	Sequence 6, Appl	C 798	9.4	52.2	20	2	US-08-256-426B-112	Sequence 112, Ap
C 726	9.6	53.3	45	2	US-08-116-778E-33	Sequence 33, Appl	799	9.4	52.2	20	2	US-08-756-806A-33	Sequence 33, Appl
C 727	9.6	53.3	45	2	US-08-438-562-33	Sequence 33, Appl	800	9.4	52.2	20	2	US-08-910-408-183	Sequence 183, Ap
C 728	9.6	53.3	45	2	US-08-483-528B-33	Sequence 33, Appl	801	9.4	52.2	20	3	US-09-143-214-33	Sequence 33, Appl
C 729	9.6	53.3	45	3	US-09-035-619-19	Sequence 19, Appl	C 802	9.4	52.2	20	3	US-09-000-136-19	Sequence 19, Appl
C 730	9.6	53.3	45	3	US-08-673-799C-33	Sequence 33, Appl	C 803	9.4	52.2	20	3	US-09-024-472-9	Sequence 9, Appl
731	9.6	53.3	45	3	US-09-091-348-13	Sequence 13, Appl	C 804	9.4	52.2	20	3	US-09-286-904-14	Sequence 54, Appl
C 732	9.6	53.3	45	3	US-09-026-958-5	Sequence 5, Appl	C 805	9.4	52.2	20	3	US-09-429-323-41	Sequence 41, Appl
C 733	9.6	53.3	45	4	US-09-514-006-19	Sequence 19, Appl	806	9.4	52.2	20	3	US-09-249-215-183	Sequence 183, Ap
C 734	9.6	53.3	45	4	US-09-393-385B-33	Sequence 33, Appl	C 807	9.4	52.2	20	4	US-09-435-266-63	Sequence 63, Appl
735	9.6	53.3	46	4	US-09-453-702B-221	Sequence 221, Ap	C 808	9.4	52.2	20	4	US-09-318-932-12	Sequence 12, Appl
C 736	9.6	53.3	47	4	US-09-338-907-335	Sequence 335, Ap	C 809	9.4	52.2	20	4	US-09-313-932-375	Sequence 375, Ap
C 737	9.6	53.3	47	4	US-09-218-207-335	Sequence 335, Ap	810	9.4	52.2	20	4	US-09-313-932-78	Sequence 78, Ap
738	9.6	53.3	47	4	US-09-641-638-1079	Sequence 1079, Ap	811	9.4	52.2	20	4	US-09-180-437-42	Sequence 42, Appl
C 739	9.6	53.3	48	2	US-08-558-269-17	Sequence 17, Appl	812	9.4	52.2	20	4	US-09-180-437-43	Sequence 43, Appl
C 740	9.6	53.3	48	2	US-08-850-049-39	Sequence 39, Appl	813	9.4	52.2	20	4	US-09-180-437-44	Sequence 44, Appl
741	9.6	53.3	48	2	US-08-050-478-39	Sequence 39, Appl	814	9.4	52.2	20	4	US-09-180-437-45	Sequence 45, Appl
C 742	9.6	53.3	48	2	US-09-198-956-26	Sequence 26, Appl	815	9.4	52.2	20	4	US-09-180-437-46	Sequence 46, Appl
C 743	9.6	53.3	48	4	US-09-198-955A-32	Sequence 32, Appl	816	9.4	52.2	20	4	US-09-180-437-47	Sequence 47, Appl
C 744	9.6	53.3	48	4	US-09-410-882-17	Sequence 17, Appl	817	9.4	52.2	20	4	US-09-180-437-48	Sequence 48, Appl
745	9.6	53.3	48	4	US-09-414-117-39	Sequence 39, Appl	818	9.4	52.2	20	4	US-09-180-437-49	Sequence 49, Appl
C 746	9.6	53.3	48	4	US-09-694-531-32	Sequence 32, Appl	819	9.4	52.2	20	4	US-09-180-437-50	Sequence 50, Appl
747	9.6	53.3	48	4	US-09-678-437-39	Sequence 39, Appl	820	9.4	52.2	20	4	US-09-487-368A-231	Sequence 231, Ap
C 748	9.6	53.3	48	4	US-09-670-141-26	Sequence 26, Appl	821	9.4	52.2	20	4	US-08-722-015A-19	Sequence 19, Appl
C 749	9.6	53.3	49	4	US-09-091-814-18	Sequence 18, Appl	C 822	9.4	52.2	20	4	US-09-702-246-65	Sequence 65, Appl
750	9.6	53.3	49	4	US-08-718-388-10	Sequence 10, Appl	C 823	9.4	52.2	20	4	US-09-506-073-35	Sequence 35, Appl
751	9.6	53.3	50	1	US-08-412-614-25	Sequence 25, Appl	C 824	9.4	52.2	20	4	US-09-640-101-54	Sequence 54, Appl
C 752	9.6	53.3	50	1	US-08-412-614-26	Sequence 26, Appl	C 825	9.4	52.2	20	4	US-09-517-657B-274	Sequence 274, Ap
C 753	9.6	53.3	50	1	US-08-412-614-27	Sequence 27, Appl	826	9.4	52.2	20	4	US-09-300-008B-3	Sequence 3, Appl
754	9.6	53.3	50	1	US-08-412-614-28	Sequence 28, Appl	C 827	9.4	52.2	20	5	PCT-US95-07111A-33	Sequence 33, Appl
C 755	9.6	53.3	50	1	US-08-470-958-9	Sequence 9, Appl	C 828	9.4	52.2	21	1	US-08-477-877B-13	Sequence 13, Appl
C 756	9.6	53.3	50	1	US-08-321-474-9	Sequence 9, Appl	C 829	9.4	52.2	21	1	US-08-472-281A-13	Sequence 13, Appl
757	9.6	53.3	50	2	US-08-635-761-25	Sequence 25, Appl	C 830	9.4	52.2	21	2	US-08-680-326-16	Sequence 16, Appl

C 831	9.4	52.2	21	2	US-08-477-989B-13	Sequence 13, Appl	904	9.4	52.2	38	2	US-08-293-620A-2087	Sequence 2087, Ap
C 832	9.4	52.2	21	2	US-09-001-826-8	Sequence 8, Appl	905	9.4	52.2	38	2	US-08-293-620A-2205	Sequence 2205, Ap
C 833	9.4	52.2	21	4	US-09-038-637-28	Sequence 28, Appl	906	9.4	52.2	38	2	US-08-292-620A-2261	Sequence 2261, Ap
C 834	9.4	52.2	21	4	US-09-038-637-60	Sequence 60, Appl	907	9.4	52.2	38	2	US-08-292-620A-2291	Sequence 2291, Ap
C 835	9.4	52.2	21	4	US-09-180-437-274	Sequence 274, Ap	908	9.4	52.2	38	2	US-09-071-845-2080	Sequence 2080, Ap
C 836	9.4	52.2	21	4	US-08-968-733-28	Sequence 28, Appl	909	9.4	52.2	38	3	US-09-071-845-2087	Sequence 2087, Ap
C 837	9.4	52.2	21	4	US-08-968-733-60	Sequence 60, Appl	910	9.4	52.2	38	3	US-09-071-845-2205	Sequence 2205, Ap
C 838	9.4	52.2	23	2	US-08-633-792A-2	Sequence 2, Appl	911	9.4	52.2	38	3	US-09-071-845-2267	Sequence 2267, Ap
C 839	9.4	52.2	23	2	US-08-853-217-14	Sequence 14, Appl	912	9.4	52.2	38	3	US-09-071-845-2291	Sequence 2291, Ap
C 840	9.4	52.2	23	4	US-09-535-006-28	Sequence 28, Appl	913	9.4	52.2	39	1	US-08-518-777-63	Sequence 63, Appl
C 841	9.4	52.2	23	4	US-08-809-297-12	Sequence 12, Appl	914	9.4	52.2	39	1	US-08-742-035-63	Sequence 63, Appl
C 842	9.4	52.2	24	7	US-08-293-814E-17	Sequence 17, Appl	915	9.4	52.2	39	1	US-08-777-019-63	Sequence 63, Appl
C 843	9.4	52.2	25	1	US-08-293-814E-33	Sequence 33, Appl	916	9.4	52.2	39	2	US-08-777-143-63	Sequence 63, Appl
C 844	9.4	52.2	25	1	US-08-871-268A-10	Sequence 10, Appl	917	9.4	52.2	39	2	US-08-775-414-63	Sequence 63, Appl
C 845	9.4	52.2	25	2	US-08-871-268B-8	Sequence 8, Appl	918	9.4	52.2	39	4	US-08-931-858E-63	Sequence 63, Appl
C 846	9.4	52.2	25	2	US-09-018-864A-8	Sequence 8, Appl	919	9.4	52.2	39	4	US-08-981-739-63	Sequence 63, Appl
C 847	9.4	52.2	25	3	US-09-343-361-17	Sequence 17, Appl	920	9.4	52.2	39	6	5175384-5	Sequence 63, Appl
C 848	9.4	52.2	25	3	US-08-871-267B-10	Sequence 10, Appl	921	9.4	52.2	39	6	5175384-5	Sequence 63, Appl
C 849	9.4	52.2	25	4	US-09-618-419-10	Sequence 10, Appl	922	9.4	52.2	39	6	5221736-7	Sequence 63, Appl
C 850	9.4	52.2	25	4	US-09-163-674-10	Sequence 10, Appl	923	9.4	52.2	40	1	US-08-741-881-84	Sequence 84, Appl
C 851	9.4	52.2	25	4	US-09-163-674-10	Sequence 10, Appl	924	9.4	52.2	40	1	US-08-738-158-84	Sequence 84, Appl
C 852	9.4	52.2	25	5	PCR-US91-02942-84	Sequence 84, Appl	925	9.4	52.2	40	1	US-08-738-158-84	Sequence 84, Appl
C 853	9.4	52.2	26	1	US-08-270-314-7	Sequence 12, Appl	926	9.4	52.2	40	2	US-08-404-796-84	Sequence 84, Appl
C 854	9.4	52.2	26	1	US-08-270-314-7	Sequence 12, Appl	927	9.4	52.2	40	3	US-08-931-868-84	Sequence 84, Appl
C 855	9.4	52.2	26	2	US-08-859-998-395	Sequence 395, App	928	9.4	52.2	40	3	US-08-931-868-84	Sequence 84, Appl
C 856	9.4	52.2	26	2	US-09-225-928-395	Sequence 7, Appl	929	9.4	52.2	40	4	US-09-185-437-73	Sequence 73, Appl
C 857	9.4	52.2	26	4	US-09-225-303-7	Sequence 12, Appl	930	9.4	52.2	40	4	US-09-350-359-84	Sequence 84, Appl
C 858	9.4	52.2	26	4	US-09-225-303-12	Sequence 235, App	931	9.4	52.2	40	4	US-08-484-932A-10	Sequence 10, Appl
C 859	9.4	52.2	27	1	US-07-977-284A-235	Sequence 1514, Ap	932	9.4	52.2	40	4	US-08-963-412-15	Sequence 15, Appl
C 860	9.4	52.2	27	2	US-08-256-426B-235	Sequence 183, Ap	933	9.4	52.2	41	3	US-08-963-412-15	Sequence 15, Appl
C 861	9.4	52.2	27	3	US-08-985-162-1514	Sequence 193, App	934	9.4	52.2	41	3	US-08-963-412-15	Sequence 15, Appl
C 862	9.4	52.2	27	3	US-08-988-099-183	Sequence 193, App	935	9.4	52.2	42	1	US-08-343-443B-50	Sequence 50, Appl
C 863	9.4	52.2	27	3	US-08-988-099-183	Sequence 193, App	936	9.4	52.2	42	2	US-09-415-785A-69	Sequence 69, Appl
C 864	9.4	52.2	27	4	US-08-253-396A-193	Sequence 3163, Ap	937	9.4	52.2	42	4	US-09-415-785A-69	Sequence 69, Appl
C 865	9.4	52.2	27	4	US-08-584-040-5318	Sequence 5218, Ap	938	9.4	52.2	42	4	US-08-944-865-59	Sequence 59, Appl
C 866	9.4	52.2	27	4	US-08-584-040-5318	Sequence 6280, Ap	939	9.4	52.2	42	4	US-08-944-865-59	Sequence 59, Appl
C 867	9.4	52.2	27	4	US-08-584-040-5318	Sequence 7044, Ap	940	9.4	52.2	42	4	US-09-415-900-59	Sequence 59, Appl
C 868	9.4	52.2	27	4	US-09-305-681-24	Sequence 24, Appl	941	9.4	52.2	42	4	US-09-415-900-59	Sequence 59, Appl
C 869	9.4	52.2	29	1	US-08-683-764-17	Sequence 17, Appl	942	9.4	52.2	43	4	US-09-459-133-19	Sequence 19, Appl
C 870	9.4	52.2	29	2	US-08-683-764-17	Sequence 22, Appl	943	9.4	52.2	43	4	US-08-938-820A-41	Sequence 41, Appl
C 871	9.4	52.2	29	2	US-08-683-764-17	Sequence 6, Appl	944	9.4	52.2	43	4	US-08-938-820A-41	Sequence 41, Appl
C 872	9.4	52.2	30	1	US-07-915-922-9	Sequence 677, Appl	945	9.4	52.2	47	1	US-08-171-389-81	Sequence 81, Appl
C 873	9.4	52.2	30	1	US-07-915-922-9	Sequence 25, Appl	946	9.4	52.2	47	1	US-08-171-389-81	Sequence 81, Appl
C 874	9.4	52.2	31	1	US-08-470-202-25	Sequence 25, Appl	947	9.4	52.2	47	2	US-08-475-228A-81	Sequence 81, Appl
C 875	9.4	52.2	31	1	US-08-470-202-25	Sequence 25, Appl	948	9.4	52.2	47	3	US-08-483-080A-81	Sequence 81, Appl
C 876	9.4	52.2	31	2	US-08-468-059-25	Sequence 25, Appl	949	9.4	52.2	47	4	US-09-354-947-81	Sequence 81, Appl
C 877	9.4	52.2	31	4	US-09-109-916-25	Sequence 25, Appl	950	9.4	52.2	47	4	US-09-641-638-197	Sequence 197, App
C 878	9.4	52.2	31	4	US-09-450-072-4	Sequence 4, Appl	951	9.4	52.2	47	4	US-09-641-638-197	Sequence 197, App
C 879	9.4	52.2	31	4	US-09-351-348-4	Sequence 11, Appl	952	9.4	52.2	47	4	US-09-641-638-197	Sequence 197, App
C 880	9.4	52.2	34	4	US-09-061-768A-11	Sequence 42, Appl	953	9.4	52.2	48	1	US-09-641-638-197	Sequence 197, App
C 881	9.4	52.2	34	4	US-08-647-924-42	Sequence 7, Appl	954	9.4	52.2	48	1	US-09-641-638-197	Sequence 197, App
C 882	9.4	52.2	35	4	US-09-581-617-7	Sequence 11, Appl	955	9.4	52.2	50	2	US-08-748-852-35	Sequence 35, Appl
C 883	9.4	52.2	36	1	US-07-914-282D-11	Sequence 11, Appl	956	9.4	52.2	50	2	US-08-748-852-35	Sequence 35, Appl
C 884	9.4	52.2	36	1	US-08-276-887A-11	Sequence 11, Appl	957	9.4	52.2	50	2	US-08-748-852-35	Sequence 35, Appl
C 885	9.4	52.2	36	1	US-08-319-492B-197	Sequence 197, Appl	958	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 886	9.4	52.2	36	1	US-08-196-538-29	Sequence 29, Appl	959	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 887	9.4	52.2	36	1	US-08-291-932A-452	Sequence 452, App	960	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 888	9.4	52.2	36	1	US-08-291-932A-452	Sequence 470, App	961	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 889	9.4	52.2	36	1	US-08-311-486C-470	Sequence 960, App	962	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 890	9.4	52.2	36	2	US-08-293-620A-960	Sequence 1022, Ap	963	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 891	9.4	52.2	36	2	US-08-293-620A-1174	Sequence 1174, Ap	964	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 892	9.4	52.2	36	2	US-08-293-620A-1174	Sequence 1174, Ap	965	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 893	9.4	52.2	36	2	US-08-585-684B-1012	Sequence 2159, Ap	966	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 894	9.4	52.2	36	2	US-08-585-684B-1012	Sequence 2159, Ap	967	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 895	9.4	52.2	36	3	US-09-071-845-960	Sequence 960, App	968	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 896	9.4	52.2	36	3	US-09-071-845-1022	Sequence 1022, Ap	969	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 897	9.4	52.2	36	3	US-09-071-845-1174	Sequence 1174, Ap	970	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 898	9.4	52.2	36	4	US-08-341-560B-21	Sequence 21, Appl	971	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 899	9.4	52.2	36	4	US-09-038-073-1012	Sequence 1012, Ap	972	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 900	9.4	52.2	36	4	US-09-038-073-1012	Sequence 1012, Ap	973	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 901	9.4	52.2	38	1	US-08-390-850-834	Sequence 834, App	974	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 902	9.4	52.2	38	1	US-08-435-634-834	Sequence 834, App	975	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl
C 903	9.4	52.2	38	2	US-08-293-620A-2080	Sequence 2080, Ap	976	9.4	52.2	50	3	US-08-828-712-6	Sequence 6, Appl

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c 977 9.2 51.1 17 2 US-08-292-620A-1980 Sequence 1980, Ap
c 978 9.2 51.1 17 2 US-08-292-620A-1982 Sequence 1982, Ap
c 979 9.2 51.1 17 3 US-07-728-220C-12 Sequence 12, Appl
c 980 9.2 51.1 17 3 US-09-071-845-1980 Sequence 1980, Ap
c 981 9.2 51.1 17 3 US-09-071-845-1982 Sequence 1982, Ap
c 982 9.2 51.1 17 4 US-08-584-040-5341 Sequence 5341, Ap
c 983 9.2 51.1 17 4 US-08-584-040-5342 Sequence 5342, Ap
c 984 9.2 51.1 17 4 US-08-584-040-5343 Sequence 5343, Ap
c 985 9.2 51.1 18 1 US-08-050-073-100 Sequence 100, App
c 986 9.2 51.1 18 1 US-08-050-073-135 Sequence 135, App
c 987 9.2 51.1 18 1 US-08-050-073-146 Sequence 146, App
c 988 9.2 51.1 18 1 US-08-050-073-208 Sequence 208, App
c 989 9.2 51.1 18 1 US-08-050-073-212 Sequence 212, App
c 990 9.2 51.1 18 1 US-08-442-061-2 Sequence 2, Appl1
c 991 9.2 51.1 18 1 US-08-363-240A-1114 Sequence 1114, Ap
c 992 9.2 51.1 18 1 US-08-363-240A-1203 Sequence 1203, Ap
c 993 9.2 51.1 18 1 US-08-363-240A-1234 Sequence 1234, Ap
c 994 9.2 51.1 18 2 US-08-117-952-129 Sequence 129, App
c 995 9.2 51.1 18 2 US-08-117-952-686 Sequence 686, App
c 996 9.2 51.1 18 2 US-08-759-581B-1 Sequence 1, Appl1
c 997 9.2 51.1 18 2 US-08-585-684B-2593 Sequence 2593, Ap
c 998 9.2 51.1 18 2 US-08-659-251-27 Sequence 27, Appl
c 999 9.2 51.1 18 2 US-09-161-015-22 Sequence 22, Appl
1000 9.2 51.1 18 3 US-09-205-921-23 Sequence 23, Appl

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ALIGNMENTS

```

RESULT 1
US-08-447-179-7/c
; Sequence 7, Application US/08447179
; Patent No. 5744303
; GENERAL INFORMATION:
; APPLICANT: Iggo, Richard
; APPLICANT: Friend, Stephen H.
; APPLICANT: Frebourg, Thierry
; APPLICANT: Ishioke, Chikashi
; TITLE OF INVENTION: FUNCTIONAL ASSAY FOR TUMOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,179
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/046,033
; FILING DATE: 12 APRIL 1993
; APPLICATION NUMBER: 07/956,696
; FILING DATE: 10 OCTOBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/159002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-447-179-7

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Query Match 83.3%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4 GGAGGCGAGCTGGC 18
Db 25 GGAAGCGAGCTGGC 11

```

```

RESULT 2
US-08-363-240A-1088/c
; Sequence 1088, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1088:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-1088

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Query Match 71.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 6.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

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Qy 2 CCGAAGCGAGCTGCG 17
Db 16 CTGAAGCGAGCTGCG 1

```

```
RESULT 3
US-08-363-240A-1184/c
; Sequence 1184, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: MCSwiggan, James
; APPLICANT: Bisgaler, Charles
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1184:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-363-240A-1184
;
Query Match 71.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 6, 5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 2 CCGAGGCGAGCTGTG 17
DB 16 CTGGAAGCGGTCTG 1
;
RESULT 4
US-08-363-240A-1087/c
; Sequence 1087, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: MCSwiggan, James
; APPLICANT: Bisgaler, Charles
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1087:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-363-240A-1087
;
Query Match 68.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 4 GGAAGCGAGCTGTG 17
DB 18 GGAAGCGGTCTG 5
;
RESULT 5
US-08-363-240A-1183/c
; Sequence 1183, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: MCSwiggan, James
; APPLICANT: Bisgaler, Charles
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/363,240A
;; FILING DATE: December 23, 1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 210/096
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; INFORMATION FOR SEQ ID NO: 1183:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-363-240A-1183

Query Match 68.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 GGAAGCAGCTCTGG 17
||| ||| ||| ||| |||
DB 18 GGAAGCAGCTCTGG 5

RESULT 6
US-09-243-335-22/c
; Sequence 22, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corp.
; APPLICANT: Susulic, Vedrana S.
; APPLICANT: Duzic, Edmir
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
; TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE
; FILE REFERENCE: 0630/0E791
; CURRENT APPLICATION NUMBER: US/09/243,335A
; CURRENT FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-243-335-22

Query Match 68.9%; Score 12.4; DB 4; Length 26;
Best Local Similarity 92.9%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GAAGCAGCTCTGG 18
||| ||| ||| ||| |||
DB 24 GAAGCAGCTCTGG 11

RESULT 7
US-09-593-589-37/c
; Sequence 37, Application US/09593589
; Patent No. 6306655
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP ALPHA EXPRESSION
; FILE REFERENCE: RTS-0119

;; CURRENT APPLICATION NUMBER: US/09/593,589
;; CURRENT FILING DATE: 2000-06-13
;; NUMBER OF SEQ ID NOS: 94
;; SEQ ID NO 37
;; LENGTH: 20
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Antisense Oligonucleotide
US-09-593-589-37

Query Match 67.8%; Score 12.2; DB 4; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCGAGGAGCTCTGG 17
||| ||| ||| ||| |||
DB 17 CCTGAGCGGAGCTCTGG 1

RESULT 8
US-08-442-010-12
; Sequence 12, Application US/08442010
; Patent No. 5849994
; GENERAL INFORMATION:
; APPLICANT: NARAYAN, Opendra
; TITLE OF INVENTION: Animal Model for HIV-1 Induced Disease
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, Ltd.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,010
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAO, MARK
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 95,645
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)715-1000
; TELEFAX: (312)715-1234
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PCR primer"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..26
; OTHER INFORMATION: /note= "complementary to B-actin"
; OTHER INFORMATION: gene
US-08-442-010-12

Query Match 67.8%; Score 12.2; DB 2; Length 26;
Best Local Similarity 82.4%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCGAGGAGCTCTGG 17
||| ||| ||| ||| |||
DB 1 CCGAGGAGGAGCTCTGG 17

RESULT 9
546668-50/c
PATENT NO. 546668
APPLICANT: GLASER, CHARLES B.; MORSE, MICHAEL J.; LIGHT,
DAVID R.
TITLE OF INVENTION: SUPERIOR THROMBOMODULIN ANALOGS FOR
PHARMACEUTICAL USE
NUMBER OF SEQUENCES: 57
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,346
FILING DATE: 22-NOV-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 568,456
FILING DATE: 15-AUG-1990
APPLICATION NUMBER: 506,325
FILING DATE: 09-APR-1990
APPLICATION NUMBER: 406,941
FILING DATE: 13-SEP-1989
APPLICATION NUMBER: 345,374
FILING DATE: 28-APR-1989
SEQ ID NO: 50:
LENGTH: 28
546668-50

Query Match
Best Local Similarity 67.8%; Score 12.2; DB 6;
Length 28;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGGAGCAGCTCGG 18
DB 18 CCGGAGCAGCTCGG 2

RESULT 10
US-08-780-949-2/c
Sequence 2, Application US/08780949
Patent No. 6002066
GENERAL INFORMATION:
APPLICANT: Leung, Wei-Ping
APPLICANT: Karlsson, Lars
APPLICANT: Zhou, Lubing
TITLE OF INVENTION: H2-M MODIFIED TRANSGENIC ANIMALS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
CITY: New Brunswick
STATE: NJ
COUNTRY: USA
ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,949
FILING DATE: 10 January 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mallen, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-819
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-524-2806
TELEFAX: 732-524-2808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ANTI-SENSE: NO
US-08-780-949-2

Query Match
Best Local Similarity 66.7%; Score 12; DB 3;
Length 23;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGCAGCTCGG 17
DB 23 AAGCAGCTCGG 12

RESULT 11
US-08-881-038A-1/c
Sequence 1, Application US/08881038A
Patent No. 6110902
GENERAL INFORMATION:
APPLICANT: Mohler, Hans
APPLICANT: Bolson, Detlev
TITLE OF INVENTION: METHODS FOR THE INHIBITION
OF NEURONAL ACTIVITY BY LOCAL DELIVERY OF ADENOSINE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 115 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,038A
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friebe, Thomas E.
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 9261-0003-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-038A-1

Query Match
Best Local Similarity 66.7%; Score 12; DB 3;
Length 26;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGCAGCTCGG 17
DB 17 AAGCAGCTCGG 6

RESULT 12
US-08-231-990-34/c
Sequence 34, Application US/08231990
Patent No. 5585232

```

: GENERAL INFORMATION:
: APPLICANT: Fair, Spencer B
: TITLE OF INVENTION: METHODS AND DIAGNOSTIC KITS FOR
: TITLE OF INVENTION: DETERMINING TOXICITY
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Neave
: STREET: 875 Third Avenue - 29th Floor
: CITY: New York City
: STATE: New York
: COUNTRY: USA
: ZIP: 10022
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/231,990
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/910,793
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Haley Jr, James F
: REGISTRATION NUMBER: 27,794
: REFERENCE/DOCKET NUMBER: Paritox-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 715-0600
: TELEFAX: (212) 715-0673
: TELEX: 14-8367
: INFORMATION FOR SEQ ID NO: 34:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 21 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-231-990-34
:
: Query Match 65.6%; Score 11.8; DB 1; Length 21;
: Best Local Similarity 86.7%; Pred. No. 2.1e+03;
: Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
:
: QY 1 CCCGGAAGCAGCTCT 15
: Db 19 CCCGGAAGCGGTTT 5
:
: RESULT 13
: US-08-367-122-34/c
: Sequence 34, Application US/08367122
: Patent No. 5589337
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: METHODS AND DIAGNOSTIC KITS FOR
: TITLE OF INVENTION: DETERMINING TOXICITY UTILIZING BACTERIAL STRESS
: NUMBER OF SEQUENCES: 54
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Neave
: STREET: 1251 Avenue of the Americas
: CITY: New York City
: STATE: New York
: COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
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: APPLICATION NUMBER: US/08/367,122
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/06537
: FILING DATE: 06-JUL-1993
: APPLICATION NUMBER: US 07/910,793
: FILING DATE: 06-JUL-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Marks, Andrew S.
: REGISTRATION NUMBER: 33,259
: REFERENCE/DOCKET NUMBER: Paritox-1 CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 596-9000
: TELEFAX: (212) 596-9090
: TELEX: 14-8367
: INFORMATION FOR SEQ ID NO: 34:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 21 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-367-122-34
:
: Query Match 65.6%; Score 11.8; DB 1; Length 21;
: Best Local Similarity 86.7%; Pred. No. 2.1e+03;
: Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
:
: QY 1 CCCGGAAGCAGCTCT 15
: Db 19 CCCGGAAGCGGTTT 5
:
: RESULT 14
: US-09-632-098-7
: Sequence 7, Application US/09632098
: Patent No. 6420154
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Balindur, Nand
: TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
: FILE REFERENCE: 99-39
: CURRENT APPLICATION NUMBER: US/09/632,098
: CURRENT FILING DATE: 2000-08-02
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 7
: LENGTH: 23
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: oligonucleotide ZC17,993
: US-09-632-098-7
:
: Query Match 65.6%; Score 11.8; DB 4; Length 23;
: Best Local Similarity 86.7%; Pred. No. 2.1e+03;
: Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
:
: QY 1 CCCGGAAGCAGCTCT 15
: Db 7 CCTGGAAGCATCTCT 21
:
: RESULT 15
: US-09-199-637A-178
: Sequence 178, Application US/09199637A
: Patent No. 6355411
: GENERAL INFORMATION:
: APPLICANT: Ausubel, Frederick
: APPLICANT: Goodman, Howard M.
: APPLICANT: Rahme, Laurence G.
: APPLICANT: Mahajan-Miklos, Shalina
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: APPLICANT: Tan, Man-Wah
: APPLICANT: Cao, Hui
: APPLICANT: Drenkard, Eliana
: APPLICANT: Tsongalis, John
: TITLE OF INVENTION: SEQUENCE-ASSOCIATED NUCLEIC ACID
: TITLE OF INVENTION: SEQUENCES AND USES THEREOF
: FILE REFERENCE: 00786/361002
: CURRENT APPLICATION NUMBER: US/09/199,637A
: PRIOR FILING DATE: 1998-11-25
: PRIOR APPLICATION NUMBER: 60/066,517
: NUMBER OF SEQ ID NOS: 437
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178
: LENGTH: 24
: TYPE: DNA
: ORGANISM: Pseudomonas aeruginosa
: US-09-199-637A-178

Query Match 65.6%; Score 11.8; DB 4; Length 24;
Best Local Similarity 86.7%; Pred. No. 2.1e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGGAGCGCAGCTGTG 16
Db 9 CCGGAGCGCAGCTGTG 23

RESULT 16
US-07-885-689A-22/C
: Sequence 22, Application US/07885689A
: Patent No. 5366876
: GENERAL INFORMATION:
: APPLICANT: Cho, Joong M.
: APPLICANT: Lee, Tae H.
: APPLICANT: Chung, Hyun H.
: APPLICANT: Lee, Yong B.
: APPLICANT: Lee, Tae G.
: APPLICANT: Park, Young W.
: APPLICANT: Han, Kyu B.
: TITLE OF INVENTION: Method for Production of Bovine Growth
: TITLE OF INVENTION: Hormone Using a Synthetic Gene.
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Birch, Stewart, Kolash & Birch
: STREET: P.O. Box 747
: CITY: Falls Church
: STATE: Virginia
: COUNTRY: USA
: ZIP: 22040-0747
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/885,689A
: FILING DATE: 19-MAY-1992
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Svensson, Leonard R.
: REGISTRATION NUMBER: 30,330
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-241-1300
: TELEFAX: 703-241-2848
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 45 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
```

```

: HYPOTHETICAL: NO
: ANTI-SENSE: YES
: FEATURE:
: NAME/KEY:
: LOCATION: 1..45
: OTHER INFORMATION: /label= oligonucleotide
: OTHER INFORMATION: /note= "L9 oligonucleotide portion of synthetic
: OTHER INFORMATION: BCH gene, Figure 1."
: US-07-885-689A-22

Query Match 65.6%; Score 11.8; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 2.1e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGAAGCGAGCTGTGCG 18
Db 20 GGAAGCGAGCTGTGCG 6

RESULT 17
US-09-253-396A-113
: Sequence 113, Application US/09253396A
: Patent No. 6205408
: GENERAL INFORMATION:
: APPLICANT: Genome Dynamics, Inc.
: TITLE OF INVENTION: DNA-Binding Proteins of the Zinc-Finger Class
: FILE REFERENCE: 1116242-0003 file: genome03f.app
: CURRENT APPLICATION NUMBER: US/09/253,396A
: CURRENT FILING DATE: 1999-02-19
: NUMBER OF SEQ ID NOS: 231
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 113
: LENGTH: 27
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
: US-09-253-396A-113

Query Match 64.4%; Score 11.6; DB 4; Length 27;
Best Local Similarity 77.8%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCGGAGCGCAGCTGTGCG 18
Db 1 CCGGAGCGCAGCTGTGCG 18

RESULT 18
US-08-840-062-12/C
: Sequence 12, Application US/08840062
: Patent No. 611977
: GENERAL INFORMATION:
: APPLICANT: LASKY, LAURENCE A.
: APPLICANT: WU, KAI
: TITLE OF INVENTION: TYPE C LECTINS
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/840,062
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Dregger, Ginger R.
```

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;
;   REGISTRATION NUMBER: 33,055
;   REFERENCE/DOCKET NUMBER: P1019R1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415/225-3216
;   TELEFAX: 415/952-9881
;   TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 29 base pairs
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
;
US-08-840-062-12
;
Query Match          64.4%; Score 11.6; DB 3; Length 29;
Best Local Similarity 77.8%; Pred. No.2.6e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCGGAGAGCAGCTGGC 18
    ||||| ||||| |||
DB 23 CCGGAGAGCAGCAGCAGC 6

RESULT 19
US-09-732-199A-22/c
; Sequence 22, Application US/09732199A
; Patent No. 6379960
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 2, P4
; FILE REFERENCE: RTS-0214
; CURRENT APPLICATION NUMBER: US/09/732,199A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 57
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-732-199A-22
;
Query Match          63.3%; Score 11.4; DB 4; Length 20;
Best Local Similarity 92.3%; Pred. No.3.2e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AAGCAGCTCTGGC 18
    ||||| ||||| |||
DB 16 AAGCAGCCTCTGGC 4

RESULT 20
US-08-370-724-6/c
; Sequence 6, Application US/08370724
; Patent No. 5972598
; GENERAL INFORMATION:
; APPLICANT: Chaudhary, Preet
; APPLICANT: Shull, Alexander
; APPLICANT: Roninson, Igor B.
; TITLE OF INVENTION: Methods for Preventing Multidrug
; TITLE OF INVENTION: Resistance in Cancer Cells
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegetti & Witcoff, Ltd.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/370,724
;   FILING DATE: 09-JAN-1995
;   CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;   NAME: No. 5972598nan, Kevin E
;   REGISTRATION NUMBER: 35,303
;   REFERENCE/DOCKET NUMBER: 95,119
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312-715-1000
;   TELEFAX: 312-715-1234
;   TELEX: 910-221-5317
;   INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 21 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;
US-08-370-724-6
;
Query Match          63.3%; Score 11.4; DB 2; Length 21;
Best Local Similarity 92.3%; Pred. No.3.2e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GAAGCAGCTCTGG 17
    ||||| ||||| |||
DB 16 GAAGCAGCTCTGG 4

RESULT 21
US-08-659-877-6/c
; Sequence 6, Application US/08659877
; Patent No. 6171786
; GENERAL INFORMATION:
; APPLICANT: Shull, Alexander
; APPLICANT: Roninson, Igor B.
; TITLE OF INVENTION: Methods for Preventing Multidrug Resistance
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegetti, Ltd.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,877
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171786nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 95,119-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: DNA (genomic)
; US-08-659-877-6
Query Match      63.3%; Score 11.4; DB 4; Length 21;
Best Local Similarity 92.3%; Pred. No. 3.2e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY      5 GAAGCAGCTCTGC 17
      |||||
Db      16 GAAGCAGCTCTGC 4

RESULT 22
US-08-328-314-7
; Sequence 7, Application US/08328314
; Patent No. 5674728
; GENERAL INFORMATION:
; APPLICANT: Buxton, Frank
; APPLICANT: Visser, Jacob
; APPLICANT: Visser, Jacob
; TITLE OF INVENTION: Fungal Protease
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,314
; FILING DATE: TBA
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spurrill, W. Murray
; REGISTRATION NUMBER: .32,943
; REFERENCE/DOCKET NUMBER: 4-19746/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8615
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..28
; OTHER INFORMATION: /standard_name= "oligonucleotide 5"
; US-08-328-314-7

Query Match      63.3%; Score 11.4; DB 1; Length 28;
Best Local Similarity 92.3%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY      6 AAGCAGCTCTGC 18
      |||||
Db      16 AAGCAGCTCTGC 28

RESULT 23
US-08-731-045-7
; Sequence 7, Application US/08731045
; Patent No. 5756338
; GENERAL INFORMATION:
; APPLICANT: Buxton, Frank
```

```
; APPLICANT: Jarai, Gabor
; APPLICANT: Visser, Jacob
; TITLE OF INVENTION: Fungal Protease
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY CORPORATION
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9725
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/731,045
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/328,314
; APPLICATION NUMBER: 08/328,314
; FILING DATE: October 24, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 4-19746/A/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-3318
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..28
; OTHER INFORMATION: /standard_name= "oligonucleotide 5"
; US-08-731-045-7

Query Match      63.3%; Score 11.4; DB 1; Length 28;
Best Local Similarity 92.3%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY      6 AAGCAGCTCTGC 18
      |||||
Db      16 AAGCAGCTCTGC 28

RESULT 24
US-08-385-191A-7/C
; Sequence 7, Application US/08385191A
; Patent No. 5821078
; GENERAL INFORMATION:
; APPLICANT: COHEN, Batya
; APPLICANT: NOVICK, Daniela
; APPLICANT: RUBINSTEIN, Menachem
; TITLE OF INVENTION: INTERFERON-ALPHA/BETA BINDING PROTEIN,
; ITS PREPARATION AND USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NETMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,191A
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,741
FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: NOVICK=7A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-385-191A-7

Query Match 63.3%; Score 11.4; DB 1; Length 38;
Best Local Similarity 92.3%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AAGCAGCTCTGCG 18
|||||
Db 38 AAGCATTCTGCG 26

RESULT 25
US-08-472-402A-7/c
Sequence 7, Application US/08472402A
Patent No. 6458932
GENERAL INFORMATION:
APPLICANT: COHEN, Batya
APPLICANT: NOVICK, Daniela
APPLICANT: RUBINSTEIN, Menachem
TITLE OF INVENTION: INTERFERON-ALPHA/BETA BINDING PROTEIN,
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,402A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/385,191
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,741
FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: NOVICK=7B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-472-402A-7

Query Match 63.3%; Score 11.4; DB 4; Length 38;
Best Local Similarity 92.3%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AAGCAGCTCTGCG 18
|||||
Db 38 AAGCATTCTGCG 26

RESULT 26
US-09-418-640-57
Sequence 57, Application US/09418640
Patent No. 6140125
GENERAL INFORMATION:
APPLICANT: Jennifer K. Taylor
TITLE OF INVENTION: ANTISENSE MODULATION OF BCL-6 EXPRESSION
FILE REFERENCE: RTS-0102
CURRENT APPLICATION NUMBER: US/09/418,640
CURRENT FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 57
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-418-640-57

Query Match 62.2%; Score 11.2; DB 3; Length 20;
Best Local Similarity 81.2%; Pred. No. 4e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGGAGGCGCTGCG 18
|||||
Db 4 CGGAGGAGGCGCTGCG 19

RESULT 27
US-09-109-663-15
Sequence 15, Application US/09109663
Patent No. 6277981
GENERAL INFORMATION:
APPLICANT: Tu, Guang-Chou
APPLICANT: Israel, Yedy
TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
FILE REFERENCE: 9855-301
CURRENT APPLICATION NUMBER: US/09/109,663
CURRENT FILING DATE: 1998-07-03
EARLIER APPLICATION NUMBER: 60/051,705
EARLIER FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Candidate
(
US-09-109-663-15

Query Match 62.2%; Score 11.2; DB 4; Length 20;
Best Local Similarity 81.2%; Pred. No. 4e+03;

```
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 CCGGAAGGAGCTCTG 17
    ||| ||| ||| |||
Db 5 CCGTAAGGAGGCTG 20

RESULT 28
US-09-173-914-34
; Sequence 34, Application US/09173914
; Patent No. 6171857
; GENERAL INFORMATION:
; APPLICANT: Hendrickson, Eric
; TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
; FILE REFERENCE: B0877/7017/HK
; CURRENT APPLICATION NUMBER: US/09/173,914
; EARLIER FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: 60/064,557
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-173-914-34

Query Match 62.2%; Score 11.2; DB 4; Length 25;
Best Local Similarity 81.2%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCGGAGGAGCTCTG 16
    ||| ||| ||| |||
Db 1 CCAGGAGTACGCTG 16

RESULT 29
US-09-593-012-129
; Sequence 129, Application US/09593012
; Patent No. 6387652
; GENERAL INFORMATION:
; APPLICANT: HAUGLAND, Richard
; APPLICANT: VESPER, Stephen
; TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
; FILE REFERENCE: HAUGLAND-1A
; CURRENT APPLICATION NUMBER: US/09/593,012
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 09/290,990
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 60/081,773
; NUMBER OF SEQ ID NOS: 225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 129
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Penicillium citrinum/sartoryi/westlingi
US-09-593-012-129

Query Match 62.2%; Score 11.2; DB 4; Length 25;
Best Local Similarity 81.2%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCGGAGGAGCTCTG 16
    ||| ||| ||| |||
Db 2 CCCTGAGGCTCTCTG 17

RESULT 30
US-09-593-012-147/c
; Sequence 147, Application US/09593012
; Patent No. 6387652

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

; GENERAL INFORMATION:
; APPLICANT: HAUGLAND, Richard
; APPLICANT: VESPER, Stephen
; TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTE
; FILE REFERENCE: HAUGLAND-1A
; CURRENT APPLICATION NUMBER: US/09/593,012
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 09/290,990
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 60/081,773
; NUMBER OF SEQ ID NOS: 225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 147
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Penicillium janthinellum/raperi
US-09-593-012-147

Query Match 62.2%; Score 11.2; DB 4; Length 25;
Best Local Similarity 81.2%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCGGAGGAGCTCTG 16
    ||| ||| ||| |||
Db 25 CCCTGAGGCTCTCTG 10

RESULT 31
US-08-259-609-12/c
; Sequence 12, Application US/08259609
; Patent No. 5989808
; GENERAL INFORMATION:
; APPLICANT: Young, Kathleen H.
; APPLICANT: Ozenberger, Bradley A.
; TITLE OF INVENTION: No. 5989808el Cell System Having Specific
; FILE REFERENCE: Interaction of Peptide Binding Pairs
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,609
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Darily L.
; REGISTRATION NUMBER: 34,276
; REFERENCE/DOCKET NUMBER: 32,352-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3247
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-259-609-12

Query Match 62.2%; Score 11.2; DB 2; Length 27;
Best Local Similarity 81.2%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY 2 CCGAAGCGAGTCTGG 17
| | | | | | | | | |
DB 25 CTGAAGCGATCTTGG 10

RESULT 32

US-09-263-944-12/c
; Sequence 12, Application US/09263944
; Patent No. 6251602

GENERAL INFORMATION:

APPLICANT: Young, Kathleen H.
APPLICANT: Ozenberger, Bradley A.
TITLE OF INVENTION: No. 6251602el Cell System Having Specific
TITLE OF INVENTION: Interaction of Peptide Binding Pairs
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,944
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,609
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Webster, Darryl L.

REGISTRATION NUMBER: 34,276

REFERENCE/DOCKET NUMBER: 32,352-00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-831-3247

TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-263-944-12

Query Match 62.2%; Score 11.2; DB 4; Length 27;
Best Local Similarity 81.2%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CCGAAGCGAGTCTGG 17
| | | | | | | | | |
DB 25 CTGAAGCGATCTTGG 10

RESULT 33

US-09-305-483-12/c
; Sequence 12, Application US/09305483
; Patent No. 6284519

GENERAL INFORMATION:

APPLICANT: Young, Kathleen H.

APPLICANT: Ozenberger, Bradley A.

TITLE OF INVENTION: No. 6284519el Cell System Having Specific

TITLE OF INVENTION: Interaction of Peptide Binding Pairs

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza

CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/305,483
FILING DATE: 06-MAY-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/259,609

FILING DATE: 14-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Webster, Darryl L.

REGISTRATION NUMBER: 34,276

REFERENCE/DOCKET NUMBER: 32,352-00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-831-3247

TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-305-483-12

Query Match 62.2%; Score 11.2; DB 4; Length 27;
Best Local Similarity 81.2%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CCGAAGCGAGTCTGG 17
| | | | | | | | | |
DB 25 CTGAAGCGATCTTGG 10

RESULT 34

US-08-446-660-7/c
; Sequence 7, Application US/08446660
; Patent No. 5723328

GENERAL INFORMATION:

APPLICANT: Dalboege, Henrik

APPLICANT: Andersen, Lene N

APPLICANT: Koefed, Lene V

APPLICANT: Kauppinen, Markus S

APPLICANT: Christgau, Stephan

TITLE OF INVENTION: AN ENZYME WITH ENDOGLUCANASE ACTIVITY

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5723328o No. 5723328disk of No. 5723328th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,660

FILING DATE: 26-MAY-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Harrington, James J.

REGISTRATION NUMBER: 38,711

REFERENCE/DOCKET NUMBER: 3950.204-US

TELECOMMUNICATION INFORMATION:

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;
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-446-660-7

Query Match
Best Local Similarity 62.2%; Score 11.2; DB 1; Length 28;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGGAGCGCAGTCTGCG 18
Db 16 CGGAGCGCAGGCTGCG 1

RESULT 35
US-08-974-302-7/c
; Sequence 7, Application US/08974302
; Patent No. 6214598
; GENERAL INFORMATION:
; APPLICANT: Dalboege, Henrik
; APPLICANT: Andersen, Lene N
; APPLICANT: Koefed, Lene V
; APPLICANT: Kuppinen, Markus S
; APPLICANT: Christgau, Stephan
; TITLE OF INVENTION: AN ENZYME WITH ENDOGLUCANASE ACTIVITY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6214598 of No. 6214598 of No. 6214598 of America, Inc.
; STREET: 405 Lexington Avenue, 64th floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,302
; FILING DATE: 19-No. 6214598ember-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeria A.35,127
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 3550,214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-974-302-7

Query Match
Best Local Similarity 62.2%; Score 11.2; DB 4; Length 28;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGGAGCGCAGTCTGCG 18
Db 16 CGGAGCGCAGGCTGCG 1

RESULT 36
US-08-216-260-11/c
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; Sequence 11, Application US/08216260
; Patent No. 5837261
; GENERAL INFORMATION:
; APPLICANT: Ingalls, Stephen C.
; APPLICANT: Boursnell, Michael E.G.
; APPLICANT: Munson, Anthony C.
; TITLE OF INVENTION: VIRAL VACCINES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobach, Test, Albritton & Herbert
; ADDRESSEE: Attn: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/216,260
; FILING DATE: 21-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9305710.7
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324964.7
; FILING DATE: 06-DEC-1993
; APPLICATION NUMBER: US 08/030,073
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 24,190
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-59886/MHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-216-260-11

Query Match
Best Local Similarity 62.2%; Score 11.2; DB 2; Length 29;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCGAGCGCAGTCTG 16
Db 17 CCCGAGCGCAATCTG 2

RESULT 37
US-08-604-165-10/c
; Sequence 10, Application US/08604165
; Patent No. 6287557
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.G.
; APPLICANT: Ingalls, Stephen C.
; TITLE OF INVENTION: Viral Preparations, Vectors,
; IMMUNOGENS, AND VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
```

ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,165
FILING DATE: 21-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9503395.7
FILING DATE: 21-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9515557.8
FILING DATE: 28-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9603322.0
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Linda R. Judge
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: A-63282/WHD/LRJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 871-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-604-165-10

Query Match 62.2%; Score 11.2; DB 4; Length 29;
Best Local Similarity 81.2%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCGAGGCACTCTG 16
DB 17 CCCGAGCAATCTG 2

RESULT 38
US-08-734-054B-10/C
Sequence 10, Application US/08734054B
Patent No. 6344445
GENERAL INFORMATION:
APPLICANT: BOURSNEILL, Michael E.G.
APPLICANT: BRENNER, Malcolm K.
APPLICANT: DILLOO, Dagmar
APPLICANT: INGILIS, Stephen C.
TITLE OF INVENTION: Herpes Virus Vectors and Their Uses
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/734,054B
FILING DATE: 18-OCT-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,649
FILING DATE: 19-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-64068/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-734-054B-10

Query Match 62.2%; Score 11.2; DB 4; Length 29;
Best Local Similarity 81.2%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCGAGGCACTCTG 16
DB 17 CCCGAGCAATCTG 2

RESULT 39
US-08-974-549A-625
Sequence 625, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:

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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 13:33:48 ; Search time 51 Seconds
(without alignments)
135.923 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 cccggaagcagctcggc 18

Scoring table: IDENTITY_NDC

Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 19255720 residues

Total number of hits satisfying chosen parameters: 177872

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	12.4	66.7	24 9 US-09-252-150-51	Sequence 51, Appl
3	11.8	65.6	17 10 US-09-866-108-1470	Sequence 1470, Ap
4	11.8	65.6	17 10 US-09-866-108-1471	Sequence 1471, Ap
5	11.8	65.6	17 10 US-09-866-108-1472	Sequence 1472, Ap
6	11.8	65.6	25 10 US-09-866-108-4399	Sequence 4399, Ap
7	11.8	65.6	25 10 US-09-866-108-4400	Sequence 4400, Ap
8	11.8	65.6	25 10 US-09-866-108-4401	Sequence 4401, Ap
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15	11.8	65.6	25 10 US-09-866-108-4408	Sequence 4408, Ap
16	11.8	65.6	25 10 US-09-866-108-4409	Sequence 4409, Ap
17	11.8	65.6	40 10 US-09-263-959-758	Sequence 758, App
18	11.6	64.4	19 9 US-10-032-495-31	Sequence 31, Appl
19	11.6	64.4	22 10 US-09-769-207A-15	Sequence 15, Appl

20	11.6	64.4	31 10 US-09-801-274-826	Sequence 826, App
21	11.6	64.4	45 10 US-09-780-669-942	Sequence 942, App
22	11.6	64.4	45 10 US-09-822-827-942	Sequence 942, App
23	11.4	63.3	28 10 US-09-825-414-81	Sequence 81, Appl
24	11.4	63.3	36 10 US-09-870-203A-25	Sequence 25, Appl
25	11.4	63.3	36 10 US-09-870-203A-26	Sequence 26, Appl
26	11.2	62.2	20 10 US-09-853-386-151	Sequence 151, App
27	11.2	62.2	21 10 US-09-765-081-41	Sequence 41, App
28	11.2	62.2	21 10 US-09-846-373B-7	Sequence 7, Appl1
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30	11.2	62.2	29 10 US-09-765-780A-10	Sequence 10, Appl
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32	11.2	62.2	36 10 US-09-727-311-25	Sequence 25, Appl
33	11.2	62.2	36 10 US-09-727-311-26	Sequence 26, Appl
34	11.2	62.2	36 10 US-09-870-203A-29	Sequence 29, Appl
35	11.2	62.2	36 10 US-09-870-203A-30	Sequence 30, Appl
36	11.2	62.2	46 10 US-09-908-599-19	Sequence 19, Appl
37	11.2	62.2	46 10 US-09-908-599-21	Sequence 21, Appl
38	11.1	61.1	27 10 US-09-817-487A-6	Sequence 6, Appl1
39	10.8	60.0	17 10 US-09-866-108-1469	Sequence 1469, Ap
40	10.8	60.0	17 10 US-09-866-108-1473	Sequence 1473, Ap
41	10.8	60.0	17 10 US-09-866-108-2211	Sequence 2211, Ap
42	10.8	60.0	17 10 US-09-866-108-2212	Sequence 2212, Ap
43	10.8	60.0	17 10 US-09-866-108-2213	Sequence 2213, Ap
44	10.8	60.0	19 10 US-09-866-108-2214	Sequence 2214, Ap
45	10.8	60.0	9 US-09-853-525-489	Sequence 489, App
46	10.8	60.0	19 10 US-09-901-244A-489	Sequence 489, App
47	10.8	60.0	21 10 US-09-723-084-71	Sequence 71, Appl
48	10.8	60.0	25 10 US-09-866-108-4398	Sequence 4398, Ap
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69	10.8	60.0	47 9 US-09-853-526-349	Sequence 349, App
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73	10.6	58.9	19 10 US-09-899-569A-24	Sequence 24, Appl
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C 157	10.2	56.7	45	10	US-09-822-827-782	Sequence 782, App
C 156	10.2	56.7	45	10	US-09-759-143-782	Sequence 782, App
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C 151	10.2	56.7	36	10	US-09-825-012-25	Sequence 25, Appl
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C 144	10.2	56.7	30	10	US-09-829-855-152	Sequence 152, App
C 143	10.2	56.7	31	10	US-09-801-274-709	Sequence 709, App
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C 132	10.2	56.7	45	10	US-09-822-827-782	Sequence 782, App
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243	9.8	54.4	21	9	US-10-103-830-2	Sequence 2, Appl1	316	9.6	53.3	21	10	US-09-990-442-455	Sequence 455, App
244	9.8	54.4	21	10	US-09-733-444-4	Sequence 4, Appl1	317	9.6	53.3	21	10	US-09-991-163-455	Sequence 455, App
245	9.8	54.4	24	10	US-09-898-570-49	Sequence 49, Appl	318	9.6	53.3	21	10	US-09-993-604-455	Sequence 455, App
246	9.8	54.4	25	9	US-09-905-291A-329	Sequence 329, App	319	9.6	53.3	21	10	US-09-990-456-455	Sequence 455, App
247	9.8	54.4	25	10	US-09-564-329A-21	Sequence 21, Appl	320	9.6	53.3	21	10	US-09-989-721-455	Sequence 455, App
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250	9.8	54.4	25	10	US-09-866-108-4119	Sequence 4119, Ap	323	9.6	53.3	23	10	US-09-909-320-411	Sequence 411, App
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252	9.8	54.4	25	10	US-09-866-108-5191	Sequence 5191, Ap	325	9.6	53.3	24	9	US-09-875-440-6	Sequence 6, Appl1
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269	9.8	54.4	25	10	US-09-963-620-21	Sequence 21, Appl	342	9.6	53.3	25	10	US-09-263-689-46	Sequence 46, Appl
270	9.8	54.4	25	10	US-09-909-068B-329	Sequence 21, Appl	343	9.6	53.3	25	10	US-09-263-689-46	Sequence 46, Appl
271	9.8	54.4	26	10	US-09-564-329A-24	Sequence 24, Appl	344	9.6	53.3	26	10	US-09-866-108-170	Sequence 170, Appl
272	9.8	54.4	26	10	US-09-854-153-24	Sequence 24, Appl	345	9.6	53.3	29	10	US-09-817-014-84	Sequence 84, Appl
273	9.8	54.4	26	10	US-09-854-153-24	Sequence 24, Appl	346	9.6	53.3	29	10	US-09-817-014-84	Sequence 84, Appl
274	9.8	54.4	26	10	US-09-854-153-24	Sequence 24, Appl	347	9.6	53.3	31	10	US-09-922-261-35	Sequence 35, Appl
275	9.8	54.4	26	10	US-09-934-773-24	Sequence 24, Appl	348	9.6	53.3	31	10	US-09-922-261-35	Sequence 35, Appl
276	9.8	54.4	26	10	US-09-963-620-24	Sequence 24, Appl	349	9.6	53.3	31	10	US-09-801-274-1138	Sequence 1138, Ap
277	9.8	54.4	26	10	US-09-729-674-228	Sequence 228, Appl	350	9.6	53.3	31	10	US-09-801-274-1138	Sequence 1138, Ap
278	9.8	54.4	31	10	US-09-801-274-230	Sequence 230, App	351	9.6	53.3	31	10	US-09-801-274-1274	Sequence 1274, Ap
279	9.8	54.4	31	10	US-09-801-274-231	Sequence 231, App	352	9.6	53.3	36	10	US-09-801-274-1274	Sequence 1274, Ap
280	9.8	54.4	31	10	US-09-801-274-1333	Sequence 411, App	353	9.6	53.3	36	10	US-09-245-487B-27	Sequence 231, Ap
281	9.8	54.4	31	10	US-09-801-274-1333	Sequence 1333, Ap	354	9.6	53.3	36	10	US-09-245-487B-27	Sequence 231, Ap
282	9.8	54.4	32	10	US-09-801-274-1401	Sequence 1401, Ap	355	9.6	53.3	36	10	US-09-946-175-33	Sequence 33, Ap
283	9.8	54.4	36	9	US-09-738-396-32	Sequence 32, Appl	356	9.6	53.3	36	10	US-09-870-203A-27	Sequence 27, Appl
284	9.8	54.4	38	10	US-10-085-519-14	Sequence 14, Appl	357	9.6	53.3	38	10	US-09-870-203A-27	Sequence 27, Appl
285	9.8	54.4	39	9	US-09-758-269-21	Sequence 21, Appl	358	9.6	53.3	39	10	US-09-993-502-6	Sequence 28, Appl
286	9.8	54.4	39	9	US-09-907-900-18	Sequence 18, Appl	359	9.6	53.3	40	10	US-09-993-502-6	Sequence 28, Appl
287	9.8	54.4	42	9	US-09-855-797A-18	Sequence 18, Appl	360	9.6	53.3	40	10	US-09-993-502-6	Sequence 28, Appl
288	9.8	54.4	42	9	US-10-027-806-86	Sequence 86, Appl	361	9.6	53.3	43	10	US-09-848-154-66	Sequence 66, Appl
289	9.8	54.4	44	10	US-09-835-659-9	Sequence 9, Appl1	362	9.6	53.3	43	10	US-09-848-154-66	Sequence 66, Appl
290	9.8	54.4	44	10	US-09-905-291A-21	Sequence 21, Appl	363	9.6	53.3	44	10	US-09-848-154-66	Sequence 66, Appl
291	9.8	54.4	44	10	US-09-905-291A-21	Sequence 21, Appl	364	9.6	53.3	44	10	US-09-848-154-66	Sequence 66, Appl
292	9.8	54.4	44	10	US-09-905-291A-21	Sequence 21, Appl	365	9.6	53.3	44	10	US-09-848-154-66	Sequence 66, Appl
293	9.8	54.4	44	10	US-09-905-291A-21	Sequence 21, Appl	366	9.6	53.3	44	10	US-09-848-154-66	Sequence 66, Appl
294	9.8	54.4	44	10	US-09-905-291A-21	Sequence 21, Appl	367	9.6	53.3	44	10	US-09-848-154-66	Sequence 66, Appl
295	9.6	53.3	17	10	US-08-375-291C-11	Sequence 11, Appl	368	9.6	53.3	48	12	US-09-853-526-335	Sequence 335, App
296	9.6	53.3	17	10	US-09-866-108-6268	Sequence 6268, Ap	369	9.6	53.3	50	10	US-09-901-484A-335	Sequence 335, App
297	9.6	53.3	17	10	US-09-866-108-6269	Sequence 6269, Ap	370	9.6	53.3	50	10	US-09-901-484A-335	Sequence 335, App
298	9.6	53.3	17	10	US-09-866-108-6269	Sequence 6269, Ap	371	9.6	53.3	50	10	US-09-901-484A-335	Sequence 335, App
299	9.6	53.3	17	10	US-09-866-108-7142	Sequence 7142, Ap	372	9.6	53.3	50	10	US-09-901-484A-335	Sequence 335, App
300	9.6	53.3	17	10	US-09-866-108-9237	Sequence 9237, Ap	373	9.6	53.3	50	10	US-09-901-484A-335	Sequence 335, App
301	9.6	53.3	17	10	US-09-866-108-9238	Sequence 9238, Ap	374	9.6	53.3	50	10	US-09-901-484A-335	Sequence 335, App
302	9.6	53.3	19	9	US-10-032-495-23	Sequence 23, Appl	375	9.6	53.3	17	9	US-09-992-598-429	Sequence 429, Appl
303	9.6	53.3	20	10	US-09-179-536B-7	Sequence 7, Appl1	376	9.6	53.3	17	10	US-09-866-108-12216	Sequence 2216, Ap
304	9.6	53.3	20	10	US-09-825-497-34	Sequence 34, Appl1	377	9.6	53.3	17	10	US-09-866-108-12217	Sequence 2217, Ap
305	9.6	53.3	20	10	US-09-796-416-7	Sequence 7, Appl1	378	9.6	53.3	17	10	US-09-866-108-12217	Sequence 2217, Ap
306	9.6	53.3	20	10	US-09-791-406-14	Sequence 14, Appl	379	9.6	53.3	17	10	US-09-866-108-12217	Sequence 2217, Ap
307	9.6	53.3	21	9	US-09-879-341-7	Sequence 7, Appl1	380	9.6	53.3	17	10	US-09-866-108-12217	Sequence 2217, Ap
308	9.6	53.3	21	9	US-09-922-598-455	Sequence 455, App	381	9.6	53.3	17	10	US-09-866-108-12217	Sequence 2217, Ap
309	9.6	53.3	21	10	US-09-765-081-337	Sequence 337, App	382	9.6	53.3	17	10	US-09-866-108-12217	Sequence 2217, Ap
310	9.6	53.3	21	10	US-09-989-723-455	Sequence 455, App	383	9.6	53.3	17	10	US-09-866-108-12217	Sequence 2217, Ap
311	9.6	53.3	21	10	US-09-989-723-455	Sequence 455, App	384	9.6	53.3	17	10	US-09-866-108-12217	Sequence 2217, Ap

C 385	9.4	52.2	17	10	US-09-989-722-429	Sequence 429, App	458	9.4	52.2	49	9	US-09-944-403-89	Sequence 89, Appl
C 386	9.4	52.2	17	10	US-09-989-723-429	Sequence 429, App	459	9.4	52.2	49	9	US-09-944-896-69	Sequence 89, Appl
C 387	9.4	52.2	17	10	US-09-989-279-429	Sequence 429, App	460	9.4	52.2	49	9	US-09-944-896-69	Sequence 89, Appl
C 388	9.4	52.2	17	10	US-09-989-727-429	Sequence 429, App	461	9.4	52.2	49	10	US-09-179-5368-119	Sequence 119, App
C 389	9.4	52.2	17	10	US-09-989-731-429	Sequence 429, App	462	9.4	52.2	49	10	US-09-866-028-89	Sequence 89, Appl
C 390	9.4	52.2	17	10	US-09-989-732-429	Sequence 429, App	463	9.4	52.2	49	10	US-09-989-122-427	Sequence 427, App
C 391	9.4	52.2	17	10	US-09-991-073-429	Sequence 429, App	464	9.4	52.2	49	10	US-09-989-723-427	Sequence 427, App
C 392	9.4	52.2	17	10	US-09-990-442-429	Sequence 429, App	465	9.4	52.2	49	10	US-09-989-723-427	Sequence 427, App
C 393	9.4	52.2	17	10	US-09-991-163-429	Sequence 429, App	466	9.4	52.2	49	10	US-09-989-723-427	Sequence 427, App
C 394	9.4	52.2	17	10	US-09-991-604-429	Sequence 429, App	467	9.4	52.2	49	10	US-09-944-449-89	Sequence 89, Appl
C 395	9.4	52.2	17	10	US-09-980-456-429	Sequence 429, App	468	9.4	52.2	49	10	US-09-989-731-427	Sequence 427, App
C 396	9.4	52.2	17	10	US-09-989-721-429	Sequence 429, App	469	9.4	52.2	49	10	US-09-944-457-89	Sequence 89, Appl
C 397	9.4	52.2	18	10	US-09-918-1864-40	Sequence 40, Appl	470	9.4	52.2	49	10	US-09-989-732-427	Sequence 427, App
C 398	9.4	52.2	18	10	US-09-918-1864-80	Sequence 80, Appl	471	9.4	52.2	49	10	US-09-991-073-427	Sequence 427, App
C 399	9.4	52.2	20	10	US-09-755-325-12	Sequence 12, Appl	472	9.4	52.2	49	10	US-09-945-687-89	Sequence 89, Appl
C 400	9.4	52.2	20	10	US-09-073-881-6	Sequence 6, Appl	473	9.4	52.2	49	10	US-09-990-442-427	Sequence 427, App
C 401	9.4	52.2	20	10	US-09-854-883-231	Sequence 231, Appl	474	9.4	52.2	49	10	US-09-991-163-427	Sequence 427, App
C 402	9.4	52.2	20	10	US-09-752-639-74	Sequence 74, Appl	475	9.4	52.2	49	10	US-09-945-015-89	Sequence 89, Appl
C 403	9.4	52.2	20	10	US-09-731-4578-83	Sequence 83, Appl	476	9.4	52.2	49	10	US-09-944-396-89	Sequence 89, Appl
C 404	9.4	52.2	20	10	US-09-984-198-74	Sequence 74, Appl	477	9.4	52.2	49	10	US-09-944-097-89	Sequence 89, Appl
C 405	9.4	52.2	20	10	US-09-797-779-6	Sequence 6, Appl	478	9.4	52.2	49	10	US-09-993-604-427	Sequence 427, App
C 406	9.4	52.2	20	10	US-09-791-243-65	Sequence 65, Appl	479	9.4	52.2	49	10	US-09-990-456-427	Sequence 427, App
C 407	9.4	52.2	21	9	US-09-803-320A-13	Sequence 13, Appl	480	9.4	52.2	49	10	US-09-944-432-89	Sequence 427, App
C 408	9.4	52.2	21	10	US-09-765-081-177	Sequence 177, App	481	9.4	52.2	49	10	US-09-943-762-89	Sequence 89, Appl
C 409	9.4	52.2	21	10	US-09-765-081-264	Sequence 264, App	482	9.4	52.2	49	10	US-09-944-654-89	Sequence 89, Appl
C 410	9.4	52.2	21	12	US-10-024-944-1	Sequence 1, Appl	483	9.4	52.2	49	10	US-09-989-721-427	Sequence 427, App
C 411	9.4	52.2	21	12	US-10-024-944-3	Sequence 3, Appl	484	9.4	52.2	49	10	US-09-943-851A-89	Sequence 427, App
C 412	9.4	52.2	22	12	US-10-024-944-2	Sequence 2, Appl	485	9.4	52.2	50	10	US-09-954-166-6	Sequence 6, Appl
C 413	9.4	52.2	24	9	US-09-959-519-5	Sequence 5, Appl	486	9.2	51.1	15	10	US-09-504-231A-1010	Sequence 1010, Ap
C 414	9.4	52.2	24	10	US-09-885-441-45	Sequence 45, Appl	487	9.2	51.1	15	10	US-09-274-533D-1010	Sequence 1010, Ap
C 415	9.4	52.2	25	10	US-09-866-108-5153	Sequence 5153, Ap	488	9.2	51.1	17	10	US-09-866-108-6266	Sequence 6266, Ap
C 416	9.4	52.2	25	10	US-09-866-108-5154	Sequence 5154, Ap	489	9.2	51.1	17	10	US-09-866-108-9221	Sequence 9227, Ap
C 417	9.4	52.2	25	10	US-09-866-108-13996	Sequence 13996, A	490	9.2	51.1	17	10	US-09-866-108-9227	Sequence 9231, Ap
C 418	9.4	52.2	25	10	US-09-866-108-13997	Sequence 13997, A	491	9.2	51.1	17	10	US-09-866-108-9231	Sequence 628, App
C 419	9.4	52.2	25	10	US-09-866-108-13998	Sequence 13998, A	492	9.2	51.1	17	10	US-09-827-998-628	Sequence 629, App
C 420	9.4	52.2	25	10	US-09-866-108-13999	Sequence 13999, A	493	9.2	51.1	17	10	US-09-827-998-629	Sequence 630, App
C 421	9.4	52.2	25	10	US-09-866-108-14000	Sequence 14000, A	494	9.2	51.1	17	10	US-09-827-998-630	Sequence 631, App
C 422	9.4	52.2	25	10	US-09-866-108-14001	Sequence 14001, A	495	9.2	51.1	17	10	US-09-827-998-631	Sequence 4, Appl
C 423	9.4	52.2	25	10	US-09-866-108-14002	Sequence 14002, A	496	9.2	51.1	19	10	US-09-805-177-4	Sequence 13, Appl
C 424	9.4	52.2	25	10	US-09-866-108-14003	Sequence 14003, A	497	9.2	51.1	19	10	US-09-985-675-13	Sequence 14, Appl
C 425	9.4	52.2	25	10	US-09-866-108-14004	Sequence 14004, A	498	9.2	51.1	20	8	US-08-375-225C-14	Sequence 90, Appl
C 426	9.4	52.2	25	10	US-09-866-108-14005	Sequence 14005, A	499	9.2	51.1	20	9	US-09-946-807-80	Sequence 90, Appl
C 427	9.4	52.2	25	10	US-09-866-108-14006	Sequence 14006, A	500	9.2	51.1	20	10	US-09-755-325-12	Sequence 12, Appl
C 428	9.4	52.2	25	10	US-09-866-108-14007	Sequence 14007, A	501	9.2	51.1	20	10	US-09-772-105-35	Sequence 35, Appl
C 429	9.4	52.2	25	10	US-09-866-108-14008	Sequence 14008, A	502	9.2	51.1	20	10	US-09-795-668-90	Sequence 90, Appl
C 430	9.4	52.2	25	10	US-09-866-108-14009	Sequence 14009, A	503	9.2	51.1	20	10	US-09-854-683-150	Sequence 150, App
C 431	9.4	52.2	25	10	US-09-866-108-14010	Sequence 14010, A	504	9.2	51.1	20	10	US-09-350-259-30	Sequence 30, Appl
C 432	9.4	52.2	25	10	US-09-866-108-14011	Sequence 14011, A	505	9.2	51.1	20	10	US-09-752-639-143	Sequence 143, App
C 433	9.4	52.2	26	12	US-10-154-801-7	Sequence 7, Appl	506	9.2	51.1	20	10	US-09-785-686-90	Sequence 90, Appl
C 434	9.4	52.2	26	12	US-10-154-801-12	Sequence 12, Appl	507	9.2	51.1	20	10	US-09-964-198-143	Sequence 143, App
C 435	9.4	52.2	27	10	US-09-738-396-38	Sequence 38, Appl	508	9.2	51.1	20	10	US-09-844-268-2	Sequence 2, Appl
C 436	9.4	52.2	29	9	US-10-125-086-6	Sequence 6, Appl	509	9.2	51.1	20	10	US-09-844-268-2	Sequence 2, Appl
C 437	9.4	52.2	29	12	US-09-729-674-250	Sequence 250, App	510	9.2	51.1	20	10	US-09-791-006-73	Sequence 73, Appl
C 438	9.4	52.2	30	12	US-10-024-944-10	Sequence 10, Appl	511	9.2	51.1	20	10	US-09-791-942-26	Sequence 26, Appl
C 439	9.4	52.2	31	9	US-09-886-136-25	Sequence 11, Appl	512	9.2	51.1	20	10	US-09-791-942-51	Sequence 51, Appl
C 440	9.4	52.2	31	9	US-09-886-150-25	Sequence 25, Appl	513	9.2	51.1	20	12	US-10-028-158-13	Sequence 13, Appl
C 441	9.4	52.2	31	10	US-09-801-274-326	Sequence 326, App	514	9.2	51.1	21	10	US-09-179-5368-50	Sequence 50, Appl
C 442	9.4	52.2	31	10	US-09-801-274-1333	Sequence 1333, Ap	515	9.2	51.1	21	10	US-09-073-881-60	Sequence 60, Appl
C 443	9.4	52.2	31	10	US-09-801-274-1482	Sequence 1482, Ap	516	9.2	51.1	21	10	US-09-994-068-8	Sequence 8, Appl
C 444	9.4	52.2	31	10	US-09-893-617-26	Sequence 26, Appl	517	9.2	51.1	22	9	US-09-988-113-36	Sequence 36, Appl
C 445	9.4	52.2	31	10	US-09-764-246-11	Sequence 11, Appl	518	9.2	51.1	22	10	US-09-899-980A-32	Sequence 32, Appl
C 446	9.4	52.2	36	10	US-09-504-231A-2740	Sequence 2740, App	519	9.2	51.1	22	10	US-09-776-874A-36	Sequence 36, Appl
C 447	9.4	52.2	36	10	US-09-274-553D-2740	Sequence 2740, Ap	520	9.2	51.1	25	10	US-09-866-108-11158	Sequence 11158, A
C 448	9.4	52.2	40	10	US-09-349-954A-14	Sequence 14, Appl	521	9.2	51.1	25	10	US-09-866-108-11159	Sequence 11159, A
C 449	9.4	52.2	40	10	US-09-907-007-14	Sequence 14, Appl	522	9.2	51.1	25	10	US-09-866-108-14119	Sequence 14119, A
C 450	9.4	52.2	41	12	US-10-024-944-7	Sequence 7, Appl	523	9.2	51.1	25	10	US-09-866-108-14131	Sequence 14131, A
C 451	9.4	52.2	41	12	US-10-024-944-8	Sequence 8, Appl	524	9.2	51.1	25	10	US-09-827-998-1443	Sequence 1443, Ap
C 452	9.4	52.2	42	10	US-09-795-006A-13	Sequence 13, Appl	525	9.2	51.1	25	10	US-09-827-998-1444	Sequence 1444, Ap
C 453	9.4	52.2	48	10	US-09-972-714-4	Sequence 4, Appl	527	9.2	51.1	25	10	US-09-827-998-1445	Sequence 1445, Ap
C 454	9.4	52.2	48	10	US-09-972-715-4	Sequence 4, Appl	528	9.2	51.1	25	10	US-09-827-998-1446	Sequence 1446, Ap
C 455	9.4	52.2	49	9	US-09-944-413-89	Sequence 89, Appl	529	9.2	51.1	25	10	US-09-827-998-1447	Sequence 1447, Ap
C 456	9.4	52.2	49	9	US-09-992-598-427	Sequence 427, App	530	9.2	51.1	25	10	US-09-827-998-1448	Sequence 1448, Ap

531	9.2	51.1	25	10	US-09-827-998-1449	Sequence 1449, Ap	C 604	9	50.0	17	10	US-09-866-108-9236	Sequence 9236, Ap
532	9.2	51.1	25	10	US-09-827-998-1450	Sequence 1450, Ap	C 605	9	50.0	17	10	US-09-866-108-10002	Sequence 10002, A
533	9.2	51.1	25	10	US-09-827-998-1451	Sequence 1451, Ap	C 606	9	50.0	17	10	US-09-866-108-10095	Sequence 10095, A
534	9.2	51.1	25	10	US-09-827-998-1452	Sequence 1452, Ap	C 607	9	50.0	18	9	US-09-944-403-44	Sequence 44, Appl
535	9.2	51.1	25	10	US-09-827-998-1453	Sequence 1453, Ap	C 608	9	50.0	18	9	US-09-944-403-44	Sequence 44, Appl
536	9.2	51.1	25	10	US-09-827-998-1454	Sequence 1454, Ap	C 609	9	50.0	18	9	US-09-944-403-44	Sequence 44, Appl
537	9.2	51.1	26	9	US-09-828-995B-47	Sequence 47, Appl	C 610	9	50.0	18	9	US-09-944-944-44	Sequence 44, Appl
538	9.2	51.1	27	10	US-09-179-536B-111	Sequence 111, Appl	C 611	9	50.0	18	10	US-09-866-028-44	Sequence 44, Appl
539	9.2	51.1	27	10	US-09-037-657-37	Sequence 37, Appl	C 612	9	50.0	18	10	US-09-944-449-44	Sequence 44, Appl
540	9.2	51.1	28	10	US-09-804-650-13	Sequence 13, Appl	C 613	9	50.0	18	10	US-09-944-457-44	Sequence 44, Appl
541	9.2	51.1	28	10	US-09-962-805-12	Sequence 12, Appl	C 614	9	50.0	18	10	US-09-945-587-44	Sequence 44, Appl
542	9.2	51.1	29	9	US-09-879-813-7	Sequence 7, Appl1	C 615	9	50.0	18	10	US-09-945-015-44	Sequence 44, Appl
543	9.2	51.1	29	9	US-09-872-209A-35	Sequence 35, Appl1	C 616	9	50.0	18	10	US-09-944-386-44	Sequence 44, Appl
544	9.2	51.1	29	10	US-09-799-964-7	Sequence 7, Appl1	C 617	9	50.0	18	10	US-09-944-097-44	Sequence 44, Appl
545	9.2	51.1	29	10	US-09-799-964-7	Sequence 7, Appl1	C 618	9	50.0	18	10	US-09-944-432-44	Sequence 44, Appl
546	9.2	51.1	30	10	US-09-962-055-39	Sequence 39, Appl	C 619	9	50.0	18	10	US-09-943-762-44	Sequence 44, Appl
547	9.2	51.1	30	10	US-09-939-119-4	Sequence 14, Appl	C 620	9	50.0	18	10	US-09-944-654-44	Sequence 44, Appl
548	9.2	51.1	30	12	US-10-023-529-39	Sequence 39, Appl	C 621	9	50.0	18	10	US-09-943-851A-44	Sequence 44, Appl
550	9.2	51.1	30	12	US-10-023-523-9	Sequence 39, Appl	C 622	9	50.0	19	9	US-10-032-495-12	Sequence 12, Appl
551	9.2	51.1	31	10	US-09-801-274-166	Sequence 166, Appl	C 623	9	50.0	19	9	US-10-032-495-27	Sequence 27, Appl
552	9.2	51.1	31	10	US-09-801-274-197	Sequence 197, Appl	C 624	9	50.0	19	9	US-09-784-199-6	Sequence 6, Appl1
553	9.2	51.1	31	10	US-09-801-274-228	Sequence 228, Appl	C 625	9	50.0	19	10	US-09-969-373-3115	Sequence 3115, Ap
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571	9.2	51.1	38	10	US-09-727-405-3	Sequence 3, Appl1	C 643	9	50.0	22	10	US-09-954-586-60	Sequence 60, Appl
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C 719	9	50.0	25	10	US-09-866-108-14889	Sequence 14889, A	792	9	50.0	48	10	US-09-945-051-115	Sequence 115, App
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C 721	9	50.0	25	10	US-09-866-108-14901	Sequence 14901, A	794	9	50.0	48	10	US-09-944-432-115	Sequence 115, App
C 722	9	50.0	25	10	US-09-866-108-14902	Sequence 14902, A	795	9	50.0	48	10	US-09-943-762-115	Sequence 115, App
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C 727	9	50.0	25	10	US-09-866-108-14991	Sequence 14991, A	C 800	8.8	48.9	50	10	US-09-751-261-9	Sequence 9, App1
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739	9	50.0	28	10	US-09-943-906-9	Sequence 9, App1	812	8.8	48.9	17	10	US-09-866-108-1376	Sequence 1376, App
740	9	50.0	29	10	US-09-949-145-32	Sequence 32, App1	813	8.8	48.9	17	10	US-09-866-108-1377	Sequence 1377, App
C 741	9	50.0	29	10	US-09-949-145-32	Sequence 32, App1	814	8.8	48.9	17	10	US-09-866-108-1378	Sequence 1378, App
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744	9	50.0	30	9	US-09-953-052-38	Sequence 38, App1	817	8.8	48.9	17	10	US-09-866-108-1475	Sequence 1475, App
745	9	50.0	30	10	US-09-795-483-14	Sequence 14, App1	818	8.8	48.9	17	10	US-09-866-108-1475	Sequence 1475, App
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877	8.8	48.9	21	10	US-09-793-686-85	Sequence 85, Appl1	950	8.8	48.9	25	10	US-09-754-167-6	Sequence 6, Appl1
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ALIGNMENTS

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; Patent No. US20020102552A1
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corp.
; APPLICANT: Susulic, Vedrana S.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
; FILE REFERENCE: 0630/0E791
; CURRENT APPLICATION NUMBER: US/09/761,116
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/243,335
; PRIOR FILING DATE: 1999-02-01
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RESULT 2
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; Patent No. US20020155604A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Brady, William A.
; APPLICANT: Grosmaire, Laura S.
; APPLICANT: Law, Che-Leung
; APPLICANT: Dua, Raj
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
; FILE REFERENCE: 9113-0019-999
; CURRENT APPLICATION NUMBER: US/09/252,150A
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: US 60/075,274
; EARLIER FILING DATE: 1998-02-19
; EARLIER APPLICATION NUMBER: US 60/108,683
; EARLIER FILING DATE: 1998-11-16
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; Sequence 1470, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yizhong
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
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US-09-866-108-1470
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; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
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; NUMBER OF SEQ ID NOS: 15752
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Query Match      65.6%; Score 11.8; DB 10; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

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QY      4  GGAGGCGAGCTGCG 18
         ||||| |||||
DB      2  GGAGGCGAGCTGCG 16
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RESULT 5
; Sequence 1472, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1472
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1472
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Query Match      65.6%; Score 11.8; DB 10; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+03;
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Matches 13: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

OY 4 GGAAGGAGCTGTGGC 18
||||| |||||
Db 1 GGAAGGAGGCTGGC 15

RESULT 6
US-09-866-108-4399
; Sequence 4399, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4399

Query Match 65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

OY 4 GGAAGGAGCTGTGGC 18
||||| |||||
Db 11 GGAAGGAGGCTGGC 25

RESULT 7
US-09-866-108-4400
; Sequence 4400, Application US/09866108

; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4400
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4400

Query Match 65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

OY 4 GGAAGGAGCTGTGGC 18
||||| |||||
Db 10 GGAAGGAGGCTGGC 24

RESULT 8
US-09-866-108-4401
; Sequence 4401, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

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FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 4401
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-4401

Query Match      65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GGAAGCAGCTGGC 18
DB      9 GGAAGCAGCTGGC 23

RESULT 9
US-09-866-108-4402
Sequence 4402, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 4402
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-4402

Query Match      65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GGAAGCAGCTGGC 18
DB      8 GGAAGCAGCTGGC 22

RESULT 10
US-09-866-108-4403
Sequence 4403, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
```

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4403
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4403
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```
Query Match 65.6%; Score 11.8; DB 10: Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
OY 4 GGAAGCAGCTGGC 18
    ||||| |||||
DB 7 GGAAGGAGGCTGGC 21
```

RESULT 11

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US-09-866-108-4404
; Sequence 4404, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
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```
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4404
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4404
```

```
Query Match 65.6%; Score 11.8; DB 10: Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 4 GGAAGCAGCTGGC 18
    ||||| |||||
DB 6 GGAAGGAGGCTGGC 20
```

RESULT 12

```
US-09-866-108-4405
; Sequence 4405, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4405
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Query Match	65.6%;	Score 11.8;	DB 10;	Length 25;
Best Local Similarity	86.7%;	Pred. No. 2.3e+03;		
Matches 13; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
OY	4	GGAGGCGAGCTGGC	18	
DB	5	GGAGGCGAGCTGGC	19	
US-09-866-108-4406				
RESULT 13				
US-09-866-108-4406				
Sequence 4406, Application US/09866108				
Patent No. US20020048800A1				
GENERAL INFORMATION:				
APPLICANT: GU, Yizhong				
APPLICANT: JI, Yonggang				
APPLICANT: PENN, Sharron G.				
APPLICANT: HANZEL, David K.				
APPLICANT: RANK, David R.				
APPLICANT: CHEN, Wensheng				
APPLICANT: SHANNON, Mark				
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE				
FILE REFERENCE: AEWICA-7				
CURRENT APPLICATION NUMBER: US/09/866,108				
CURRENT FILING DATE: 2001-05-25				
PRIOR APPLICATION NUMBER: US 60/207,456				
PRIOR FILING DATE: 2000-05-26				
PRIOR APPLICATION NUMBER: GB 24263.6				
PRIOR FILING DATE: 2000-10-04				
PRIOR APPLICATION NUMBER: US 60/236,359				
PRIOR FILING DATE: 2000-09-27				
PRIOR APPLICATION NUMBER: PCT/US01/00666				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00667				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00664				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00669				
PRIOR FILING DATE: 2001-01-30				
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PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00668				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00663				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00662				
PRIOR FILING DATE: 2000-09-21				
PRIOR APPLICATION NUMBER: US 60/266,860				
PRIOR FILING DATE: 2001-02-05				
NUMBER OF SEQ ID NOS: 15752				
SOFTWARE: Aecomica Sequence Listing Engine				
SEQ ID NO 4406				
LENGTH: 25				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-09-866-108-4406				
Query Match				
US-09-866-108-4406				
Sequence 4408, Application US/09866108				
Patent No. US20020048800A1				
GENERAL INFORMATION:				
APPLICANT: GU, Yizhong				
APPLICANT: JI, Yonggang				
APPLICANT: PENN, Sharron G.				
APPLICANT: HANZEL, David K.				
APPLICANT: RANK, David R.				
APPLICANT: CHEN, Wensheng				
APPLICANT: SHANNON, Mark				
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE				
FILE REFERENCE: AEWICA-7				
CURRENT APPLICATION NUMBER: US/09/866,108				
CURRENT FILING DATE: 2001-05-25				
PRIOR APPLICATION NUMBER: US 60/207,456				
PRIOR FILING DATE: 2000-05-26				
PRIOR APPLICATION NUMBER: GB 24263.6				
PRIOR FILING DATE: 2000-10-04				
PRIOR APPLICATION NUMBER: US 60/236,359				
PRIOR FILING DATE: 2000-09-27				
PRIOR APPLICATION NUMBER: PCT/US01/00666				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00667				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00664				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00669				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00665				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00668				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00663				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00662				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00661				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00670				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: US 60/234,687				
PRIOR FILING DATE: 2000-09-21				
PRIOR APPLICATION NUMBER: US 60/266,860				
PRIOR FILING DATE: 2001-02-05				
NUMBER OF SEQ ID NOS: 15752				
SOFTWARE: Aecomica Sequence Listing Engine				
SEQ ID NO 4407				
LENGTH: 25				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-09-866-108-4407				
Query Match				
US-09-866-108-4407				
Sequence 4407, Application US/09866108				
Patent No. US20020048800A1				
GENERAL INFORMATION:				
APPLICANT: GU, Yizhong				
APPLICANT: JI, Yonggang				
APPLICANT: PENN, Sharron G.				
APPLICANT: HANZEL, David K.				
APPLICANT: RANK, David R.				
APPLICANT: CHEN, Wensheng				
APPLICANT: SHANNON, Mark				
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE				
FILE REFERENCE: AEWICA-7				
CURRENT APPLICATION NUMBER: US/09/866,108				
CURRENT FILING DATE: 2001-05-25				
PRIOR APPLICATION NUMBER: US 60/207,456				
PRIOR FILING DATE: 2000-05-26				
PRIOR APPLICATION NUMBER: GB 24263.6				
PRIOR FILING DATE: 2000-10-04				
PRIOR APPLICATION NUMBER: US 60/236,359				
PRIOR FILING DATE: 2000-09-27				
PRIOR APPLICATION NUMBER: PCT/US01/00666				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00667				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00664				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00669				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00665				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00668				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00663				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00662				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00661				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: PCT/US01/00670				
PRIOR FILING DATE: 2001-01-30				
PRIOR APPLICATION NUMBER: US 60/234,687				
PRIOR FILING DATE: 2000-09-21				
PRI				

```
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4408
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4408

Query Match      65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      4 GGAAGCAGCTGCGC 18
        ||||| |||||
Db      2 GGAAGGAGGCGCTGC 16

RESULT 16
US-09-866-108-4409
; Sequence 4409, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
```

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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4409
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4409

Query Match      65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      4 GGAAGCAGCTGCGC 18
        ||||| |||||
Db      1 GGAAGGAGGCGCTGC 15

RESULT 17
US-09-263-959-758/C
; Sequence 758, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: KOOP, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
```

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TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 758:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-758

Query Match          65.6%; Score 11.8; DB 10; Length 40;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGAAGCAGCTCTGGC 18
    |||||
DB 39 GGAAGCAGCAGCGC 25

RESULT 18
US-10-032-495-31/c
; Sequence 31, Application US/10032495
; Patent No. US20020155601A1
; GENERAL INFORMATION:
; APPLICANT: YAN, WEN LIANG
; TITLE OF INVENTION: METHOD FOR PRODUCING A POPULATION OF HOMOZYGOUS STEM
; TITLE OF INVENTION: CELLS HAVING A PRE-SELECTED IMMUNOTYPE AND/OR GENOTYPE,
; TITLE OF INVENTION: CELLS SUITABLE FOR TRANSPLANT DERIVED THEREFROM, AND
; TITLE OF INVENTION: MATERIALS AND METHODS USING SAME
; FILE REFERENCE: 0249-0002US
; CURRENT APPLICATION NUMBER: US/10/032,495
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 60/258,881
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-032-495-31

Query Match          64.4%; Score 11.6; DB 9; Length 19;
Best Local Similarity 77.8%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGAGGCGACTCTGGC 18
    |||||
DB 19 CCTGAGAGACAGCGCGC 2

RESULT 19
US-09-769-207A-15
; Sequence 15, Application US/09769207A
; Patent No. US20020132234A1
; GENERAL INFORMATION:
; APPLICANT: DZGenes, LLC
; TITLE OF INVENTION: NITRIC OXIDE SYNTHASE GENE DIAGNOSTIC POLYMORPHISMS
; FILE REFERENCE: DZG 2165.1
; CURRENT APPLICATION NUMBER: US/09/769,207A
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/117,775
; PRIOR FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: US 60/220,662
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 15
; LENGTH: 22
; TYPE: DNA
```

```
ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Misc_feature
; LOCATION: (1)-(22)
; OTHER INFORMATION: STAT_1 (Se-Cys tRNA gene transcription activating factor)
US-09-769-207A-15

Query Match          64.4%; Score 11.6; DB 10; Length 22;
Best Local Similarity 77.8%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGAGGCGACTCTGGC 18
    |||||
DB 5 CCCAGCATGCACCTCTGGC 22

RESULT 20
US-09-801-274-826
; Sequence 826, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 826
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-826

Query Match          64.4%; Score 11.6; DB 10; Length 31;
Best Local Similarity 77.8%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGAGGCGACTCTGGC 18
    |||||
DB 12 CCTTAAAGCGCGGCTGGC 29

RESULT 21
US-09-780-669-942/c
; Sequence 942, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
```

```
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 942
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-942

Query Match
Best Local Similarity 64.4%; Score 11.6; DB 10; Length 45;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGAGGCGACTGTGCC 18
Db 30 CACGCTAGGCATTCTGCC 13

RESULT 22
US-09-822-827-942/C
; Sequence 942, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 942
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-942

Query Match
Best Local Similarity 64.4%; Score 11.6; DB 10; Length 45;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGAGGCGACTGTGCC 18
Db 30 CACGCTAGGCATTCTGCC 13

RESULT 23
US-09-825-414-81/C
; Sequence 81, Application US/09825414
; Patent No. US20020083489A1
; GENERAL INFORMATION:
; APPLICANT: Collier, Alan
; APPLICANT: Alfano, James R.
; APPLICANT: Charkowski, Amy O.
; TITLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE
; TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
; FILE REFERENCE: 19603/3243
; CURRENT APPLICATION NUMBER: US/09/825,414
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,160
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/224,604
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/249,548
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
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```
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-825-414-81

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 10; Length 28;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCGAGGCGAGTC 14
Db 26 CTGGAAGCGAGTC 14

RESULT 24
US-09-870-203A-25
; Sequence 25, Application US/09870203A
; Patent No. US20020137213A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020137213A1art1s AG
; TITLE OF INVENTION: Adenovirus particles with mutagenized fiber proteins
; FILE REFERENCE: 4-31452A
; CURRENT APPLICATION NUMBER: US/09/870,203A
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
; NAME/KEY: primer_bind
; LOCATION: (1)..(36)
; OTHER INFORMATION:
US-09-870-203A-25

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 10; Length 36;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AAGCGAGCTGTGCC 18
Db 20 AAGCGAGCTGTGCC 32

RESULT 25
US-09-870-203A-26/C
; Sequence 26, Application US/09870203A
; Patent No. US20020137213A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020137213A1art1s AG
; TITLE OF INVENTION: Adenovirus particles with mutagenized fiber proteins
; FILE REFERENCE: 4-31452A
; CURRENT APPLICATION NUMBER: US/09/870,203A
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
; NAME/KEY: primer_bind
; LOCATION: (1)..(36)
; OTHER INFORMATION:
US-09-870-203A-26

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 10; Length 36;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Matches 12: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AAGGCACTGTGGC 18
| | | | | | | | | |
Db 17 AAGGCACTGTGGC 5

RESULT 26

US-09-853-386-151/C
; Sequence 151, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Evelyn
; APPLICANT: Bresnahan, Barry
; APPLICANT: Conneely, Orla
; APPLICANT: Fitzgerald, Oliver
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NMR
; FILE REFERENCE: P01972051
; CURRENT APPLICATION NUMBER: US/09/853,386
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203645
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 151
; LENGTH: 20
; TYPE: DNA
; ORGANISM: HUMAN
US-09-853-386-151

Query Match 62.2%; Score 11.2; DB 10; Length 20;
Best Local Similarity 81.2%; Pred. No. 4.5e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CCGGAAGCAGCTGG 17
| | | | | | | | | |
Db 16 CAGGAAGCAGCTGAG 1

RESULT 27

US-09-765-081-41/C
; Sequence 41, Application US/09765081
; Patent No. US20020037508A1
; GENERAL INFORMATION:
; APPLICANT: Carrigill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825,2008-001
; CURRENT APPLICATION NUMBER: US/09/765,081
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,861
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-765-081-41

Query Match 62.2%; Score 11.2; DB 10; Length 21;
Best Local Similarity 72.2%; Pred. No. 4.5e+03;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCGGAAGCAGCTGGC 18
| | | | | | | | | |
Db 21 CCTGATATATGTCTGCG 4

RESULT 28
US-09-846-573B-7/c

; Sequence 7, Application US/09846573B
; Patent No. US20020077467A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Moore, Emma E.
; APPLICANT: Raymond, Penella
; TITLE OF INVENTION: Mammalian Calcitonin-Like Polypeptide-1
; FILE REFERENCE: 97-73C1
; CURRENT APPLICATION NUMBER: US/09/846,573B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/213,634
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/069,976
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-846-573B-7

Query Match 62.2%; Score 11.2; DB 10; Length 21;
Best Local Similarity 81.2%; Pred. No. 4.5e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CCGGAAGCAGCTGG 17
| | | | | | | | | |
Db 19 CCGGAAGTATGTGCG 4

RESULT 29
US-09-235-594-7/c
; Sequence 7, Application US/09235594
; Patent No. US20010014659A1
; GENERAL INFORMATION:
; APPLICANT: Convents, Andre C.
; APPLICANT: Moese, Rosa Laura
; TITLE OF INVENTION: LAUNDRY AND CLEANING COMPOSITIONS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY
; STREET: 11810 East Miami River Road
; CITY: Ross
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,594
; FILING DATE: January 22, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cook, C. Brant
; REGISTRATION NUMBER: 39,151
; REFERENCE/DOCKET NUMBER: 6613
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-0032
; TELEFAX: (513) 627-0318
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-235-594-7

Query Match 62.2%; Score 11.2; DB 10; Length 28;
Best Local Similarity 81.2%; Pred. No. 4.6e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CGGAGGAGCTCTGC 18
DB 16 CGGAGCGAGGCTGC 1

RESULT 30
US-09-765-780A-10/C
; Sequence 10, Application US/09765780A
; Patent No. US20020021298A1
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.G.
; Inglis, Stephen C.
; TITLE OF INVENTION: Viral Preparations, Vectors,
; Immunogens, and Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,780A
; FILING DATE: 19-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,165
; FILING DATE: 1996-02-21
; APPLICATION NUMBER: GB 9515557.8
; FILING DATE: 28-JUL-1995
; APPLICATION NUMBER: GB 9603322.0
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda R. Judge
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: A-63282/WHD/LRJ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 871-1989
; TELEFAX: (415) 949-8711
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-765-780A-10

Query Match 62.2%; Score 11.2; DB 10; Length 29;
Best Local Similarity 81.2%; Pred. No. 4.6e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCGAGGAGCTCTG 16
DB 17 CCCGAGCAATCTG 2

RESULT 31
US-09-765-870-10/C
; Sequence 10, Application US/09765870
; Patent No. US20020150562A1
; GENERAL INFORMATION:

APPLICANT: Boursnell, Michael E.G.
; Inglis, Stephen C.
; TITLE OF INVENTION: Viral Preparations, Vectors,
; Immunogens, and
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,870
; FILING DATE: 19-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,165
; FILING DATE: 1996-02-21
; APPLICATION NUMBER: GB 9515557.8
; FILING DATE: 28-JUL-1995
; APPLICATION NUMBER: GB 9603322.0
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda R. Judge
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: A-63282/WHD/LRJ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 871-1989
; TELEFAX: (415) 949-8711
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-765-870-10

Query Match 62.2%; Score 11.2; DB 10; Length 29;
Best Local Similarity 81.2%; Pred. No. 4.6e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCGAGGAGCTCTG 16
DB 17 CCCGAGCAATCTG 2

RESULT 32
US-09-727-311-25
; Sequence 25, Application US/09727311
; Patent No. US20010024782A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; RANDOMIZED PEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/727,311
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/767,436
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P31 9072
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 25:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 36 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-09-727-311-25
:
Query Match          62.2%; Score 11.2; DB 10; Length 36;
Best Local Similarity 81.2%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGAAGCGAGTCTGCG 17
DB 12 CCGATGGAATTCGCG 27

RESULT 33
US-09-727-311-36
: Sequence 36, Application US/09727311
: Patent No. US20010024782A1
: GENERAL INFORMATION:
: APPLICANT: Huse, William D.
: TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
: TITLE OF INVENTION: RANDOMIZED PEPTIDES
: NUMBER OF SEQUENCES: 61
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
: STREET: 444 South Flower Street, Suite 2000
: CITY: Los Angeles
: STATE: California
: COUNTRY: United States
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/727,311
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/767,436
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P31 9072
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 36 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
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: TOPOLOGY: linear
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US-09-727-311-36
:
Query Match          62.2%; Score 11.2; DB 10; Length 36;
Best Local Similarity 81.2%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGAAGCGAGTCTGCG 17
DB 12 CCGATGGAATTCGCG 27

RESULT 34
US-09-870-203A-29
: Sequence 29, Application US/09870203A
: Patent No. US20020137213A1
: GENERAL INFORMATION:
: APPLICANT: NO. US20020137213A1artis AG
: TITLE OF INVENTION: Adenovirus particles with mutagenized fiber proteins
: FILE REFERENCE: 4-31452A
: CURRENT APPLICATION NUMBER: US/09/870,203A
: CURRENT FILING DATE: 2001-05-30
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: Patentin version 3.1
: SEQ ID NO: 29
: LENGTH: 36
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: PCR primer
: NAME/KEY: primer_bind
: LOCATION: (1)..(36)
: OTHER INFORMATION:
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US-09-870-203A-29
:
Query Match          62.2%; Score 11.2; DB 10; Length 36;
Best Local Similarity 81.2%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCGAAGCGAGTCTGCG 18
DB 17 CTGACGAGCGATTGCG 32

RESULT 35
US-09-870-203A-30/C
: Sequence 30, Application US/09870203A
: Patent No. US20020137213A1
: GENERAL INFORMATION:
: APPLICANT: NO. US20020137213A1artis AG
: TITLE OF INVENTION: Adenovirus particles with mutagenized fiber proteins
: FILE REFERENCE: 4-31452A
: CURRENT APPLICATION NUMBER: US/09/870,203A
: CURRENT FILING DATE: 2001-05-30
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: Patentin version 3.1
: SEQ ID NO: 30
: LENGTH: 36
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: PCR primer
: NAME/KEY: primer_bind
: LOCATION: (1)..(36)
: OTHER INFORMATION:
:
US-09-870-203A-30
:
Query Match          62.2%; Score 11.2; DB 10; Length 36;
Best Local Similarity 81.2%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCGAAGCGAGTCTGCG 18
DB 17 CTGACGAGCGATTGCG 32
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DB      20 CTCGAGCAGCTTGGC 5

RESULT 36
US-09-908-599-19/c
; Sequence 19, Application US/09908599
; Patent No. US2002005147A1
; GENERAL INFORMATION:
; APPLICANT: LI, Haodong et al.
; TITLE OF INVENTION: Human Chemokine Beta 13
; FILE REFERENCE: PF177P3
; CURRENT APPLICATION NUMBER: US/09/908,599
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/432,768
; PRIOR FILING DATE: 1999-11-03
; PRIOR APPLICATION NUMBER: 60/032,432
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-599-19

Query Match
Best Local Similarity 62.2%; Score 11.2; DB 10; Length 46;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCCGGAAGCAGCTCG 16
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DB      46 CCAGGAGTGCAGCTCG 31

RESULT 37
US-09-908-599-21/c
; Sequence 21, Application US/09908599
; Patent No. US2002005147A1
; GENERAL INFORMATION:
; APPLICANT: LI, Haodong et al.
; TITLE OF INVENTION: Human Chemokine Beta 13
; FILE REFERENCE: PF177P3
; CURRENT APPLICATION NUMBER: US/09/908,599
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/432,768
; PRIOR FILING DATE: 1999-11-03
; PRIOR APPLICATION NUMBER: 60/032,432
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-599-21

Query Match
Best Local Similarity 62.2%; Score 11.2; DB 10; Length 46;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCCGGAAGCAGCTCG 16
        ||||| |||||
DB      46 CCAGGAGTGCAGCTCG 31

RESULT 38
US-09-817-487A-6/c
; Sequence 6, Application US/09817487A
; Patent No. US20020150876A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020150876A1artis AG
; TITLE OF INVENTION: Selectable Marker Genes
; FILE REFERENCE: 4-31193A
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; CURRENT APPLICATION NUMBER: US/09/817,487A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-817-487A-6

Query Match
Best Local Similarity 61.1%; Score 11; DB 10; Length 27;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 GGCAGTCTGGC 18
        |||||
DB      19 GGCAGTCTGGC 9

RESULT 39
US-09-866-108-1469
; Sequence 1469, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1469
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1469
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Job time : 59 secs

Query Match 60.0%: Score 10.8; DB 10: Length 17;
Best Local Similarity 85.7%: Pred. No. 7, 1e+03;
Matches 12: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GAAGGAGCTGCG 17
||||| |||||
DB 4 GAAGGAGGCTGCG 17

RESULT 40

US-09-866-108-1473
Sequence 1473, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AROMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1473
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-1473

Query Match 60.0%: Score 10.8; DB 10: Length 17;
Best Local Similarity 85.7%: Pred. No. 7, 1e+03;
Matches 12: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 GAAGGAGCTGCG 18
||||| |||||
DB 1 GAAGGAGGCTGCG 14

Search completed: December 2, 2002, 15:02:17

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 12:42:48 ; Search time 1922 Seconds
(without alignments)
151.675 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 cccggaagcagctctgac 18

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:*
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3: em_estlu:*
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5: em_estov:*
6: em_estpi:*
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8: em_estri:*
9: gb_estl:*
10: gb_estl2:*
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13: gb_estl5:*
14: gb_estl6:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_fov:*
20: em_gss_pln:*
21: em_gss_rtc:*
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27: em_gss_rtc7:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.4	74.4	43	9	A1786712 u55b03.x
2	13.2	73.3	40	9	A1111398 mp10f06.1
3	12.2	67.8	36	13	B1246232 602958773
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5	11.8	65.6	32	17	A2824475 2M0095001
6	11.8	65.6	42	9	AA975650 oq63d09.s

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8	11.6	64.4	42	13	B1252223
9	11.6	64.4	42	13	B1252248
10	11.6	64.4	45	17	B1252948
11	11.6	64.4	50	9	CNS07HVN
12	11.6	64.4	50	9	AU102427
13	11.6	64.4	50	9	AU102430
14	11.2	62.2	22	17	A2821049
15	11.2	62.2	22	17	A276661
16	11.2	62.2	50	9	AU104235
17	11.2	62.2	50	9	AU104249
18	11.2	62.2	50	9	AU107251
19	10.8	60.0	38	17	A2874759
20	10.8	60.0	42	17	A2911289
21	10.8	60.0	43	17	AL771267
22	10.8	60.0	46	17	W05609
23	10.8	60.0	49	9	AA863626
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25	10.8	60.0	50	14	R82988
26	10.6	58.9	29	17	AU107138
27	10.6	58.9	31	14	A2610133
28	10.6	58.9	31	14	T62015
29	10.6	58.9	38	17	A2953906
30	10.6	58.9	42	17	AQ939867
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32	10.6	58.9	43	14	H63217
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34	10.6	58.9	49	9	AA185949
35	10.6	58.9	50	9	AU108079
36	10.4	57.8	50	12	BQ296675
37	10.4	57.8	22	17	A2486623
38	10.4	57.8	33	17	A2595064
39	10.4	57.8	33	17	A2318942
40	10.4	57.8	35	17	A2313241
41	10.4	57.8	35	17	A2607760
42	10.4	57.8	46	9	AA846083
43	10.4	57.8	46	9	AA561711
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52	10.2	56.7	38	17	A2786726
53	10.2	56.7	44	10	H23232
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65	10.2	56.7	50	9	AU103035
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75	10.2	56.7	50	9	AU103035
76	10.2	56.7	50	9	AU103035
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82	10	55.6	49	14	W77746	W77746	z669a04.r.1	155	9.6	53.3	49	13	BM284293	BM284293	k132e05.y
83	10	55.6	50	9	AU103727	AU103727	AU103727	156	9.6	53.3	49	17	TA178E05Q	TA178E05Q	At474011 T. brucei
84	10	55.6	50	9	AU104217	AU104217	AU104217	157	9.6	53.3	50	9	AU102828	AU102828	AU102828
85	10	55.6	50	9	AU104219	AU104219	AU104219	158	9.6	53.3	50	9	AU102829	AU102829	AU102829
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C 87	10	55.6	50	9	AU106288	AU106288	AU106288	160	9.6	53.3	50	9	AU103166	AU103166	AU103166
C 88	10	55.6	50	9	AU106292	AU106292	AU106292	161	9.6	53.3	50	9	AU103373	AU103373	AU103373
C 89	10	55.6	50	9	AU107361	AU107361	AU107361	162	9.6	53.3	50	9	AU103889	AU103889	AU103889
C 90	10	55.6	50	9	AU108009	AU108009	AU108009	163	9.6	53.3	50	9	AU104945	AU104945	AU104945
C 91	10	55.6	50	10	BB616279	BB616279	BB616279	164	9.6	53.3	50	9	AU105844	AU105844	AU105844
C 92	10	55.6	22	17	AZ776605	AZ776605	2M0010119	165	9.6	53.3	50	9	AU105859	AU105859	AU105859
C 93	9.8	54.4	23	17	AZ659392	AZ659392	1M0536C13	166	9.6	53.3	50	9	AU106634	AU106634	AU106634
C 94	9.8	54.4	25	17	BH854637	BH854637	KG07068-5	167	9.6	53.3	50	9	AU106636	AU106636	AU106636
C 95	9.8	54.4	28	17	AA916534	AA916534	on64g01.s	168	9.6	53.3	50	9	AU107987	AU107987	AU107987
C 96	9.8	54.4	38	17	AZ440668	AZ440668	1M0231A20	169	9.6	53.3	50	9	AU107988	AU107988	AU107988
C 97	9.8	54.4	39	17	AZ592385	AZ592385	1M0403H14	170	9.6	53.3	50	9	AU107996	AU107996	AU107996
C 98	9.8	54.4	39	17	AZ592385	AZ592385	1M0403H14	171	9.6	53.3	50	14	T82724	T82724	N19006 Aspe
C 99	9.8	54.4	40	9	AA990516	AA990516	uA63g05.s	172	9.4	52.2	22	17	AZ372259	AZ372259	IM0124J02
C 100	9.8	54.4	42	10	AV833675	AV833675	AV833675	173	9.4	52.2	26	17	AZ462630	AZ462630	1M0269F08
C 101	9.8	54.4	44	9	A1256664	A1256664	u129H04.Y	174	9.4	52.2	27	17	AZ792197	AZ792197	2M0043C04
C 102	9.8	54.4	44	12	BF792517	BF792517	602253C26	175	9.4	52.2	28	17	AZ759986	AZ759986	1M0553115
C 103	9.8	54.4	44	13	BT106206	BT106206	602890810	176	9.4	52.2	30	17	AZ463716	AZ463716	1M0272D14
C 104	9.8	54.4	44	17	AZ814521	AZ814521	2M0082J14	177	9.4	52.2	34	13	B1690808	B1690808	603312134
C 105	9.8	54.4	46	17	AZ501017	AZ501017	1M0339L07	178	9.4	52.2	36	12	B6699624	B6699624	602679355
C 106	9.8	54.4	48	17	AZ779115	AZ779115	2M0012113	179	9.4	52.2	37	9	AA680722	AA680722	LMFPM022
C 107	9.8	54.4	48	17	BH866303	BH866303	SALK_1011	180	9.4	52.2	37	17	AZ312298	AZ312298	1M0028L02
C 108	9.8	54.4	49	9	A1154153	A1154153	wd78g01.r	181	9.4	52.2	37	17	AZ662400	AZ662400	1M0541N02
C 109	9.8	54.4	49	17	AZ606700	AZ606700	1M0428E15	182	9.4	52.2	39	9	AL787864	AL787864	AL787864
C 110	9.8	54.4	50	9	AU103386	AU103386	AU103386	183	9.4	52.2	39	17	AZ312458	AZ312458	1M0028L18
C 111	9.8	54.4	50	9	AU103856	AU103856	AU103856	184	9.4	52.2	40	17	AZ664676	AZ664676	1M0545M04
C 112	9.8	54.4	50	9	AU104350	AU104350	AU104350	185	9.4	52.2	40	17	AL770086	AL770086	ArAb1dops
C 113	9.8	54.4	50	9	AU107388	AU107388	AU107388	186	9.4	52.2	41	17	AZ658005	AZ658005	1M0534J03
C 114	9.8	54.4	50	9	AU107901	AU107901	AU107901	187	9.4	52.2	41	17	AZ663826	AZ663826	1M0543I08
C 115	9.8	54.4	50	9	AU108030	AU108030	AU108030	188	9.4	52.2	42	13	B1049432	B1049432	B1049432
C 116	9.8	54.4	50	9	AU108031	AU108031	AU108031	189	9.4	52.2	43	13	B6701002	B6701002	602864283
C 117	9.8	54.4	50	9	AU108032	AU108032	AU108032	190	9.4	52.2	46	9	AU259626	AU259626	AU259626
C 118	9.8	54.4	50	10	AM249795	AM249795	2819197.3	191	9.4	52.2	47	17	AZ845343	AZ845343	2M0145B07
C 119	9.8	54.4	50	17	AZ781441	AZ781441	2M0019N14	192	9.4	52.2	47	17	TA132E04P	TA132E04P	TA132E04P
C 120	9.8	54.4	50	17	BH644632	BH644632	1M00053H0	193	9.4	52.2	49	9	AA157965	AA157965	z054h01.s
C 121	9.8	54.4	50	17	BH847539	BH847539	SALK_0547	194	9.4	52.2	50	9	AU102826	AU102826	AU102826
C 122	9.6	53.3	22	9	AA911591	AA911591	od90D07.s	195	9.4	52.2	50	9	AU103596	AU103596	AU103596
C 123	9.6	53.3	23	17	AZ822715	AZ822715	2M0096M10	196	9.4	52.2	50	9	AU103598	AU103598	AU103598
C 124	9.6	53.3	24	17	AZ449783	AZ449783	1M0248M07	197	9.4	52.2	50	9	AU104493	AU104493	AU104493
C 125	9.6	53.3	26	17	AZ623015	AZ623015	1M0460P14	198	9.4	52.2	50	9	AU104699	AU104699	AU104699
C 126	9.6	53.3	28	9	AA856526	AA856526	vx02g12.r	199	9.4	52.2	50	9	AU105508	AU105508	AU105508
C 127	9.6	53.3	28	9	AA484974	AA484974	aa39a01.r	200	9.4	52.2	50	9	AU105633	AU105633	AU105633
C 128	9.6	53.3	28	17	BH848015	BH848015	SALK_0673	201	9.4	52.2	50	9	AU106503	AU106503	AU106503
C 129	9.6	53.3	31	9	A1493525	A1493525	qy96c11.x	202	9.4	52.2	50	9	AU106751	AU106751	AU106751
C 130	9.6	53.3	32	14	T67801	T67801	yc39a09..s1	203	9.4	52.2	50	9	AU106753	AU106753	AU106753
C 131	9.6	53.3	33	12	BG529354	BG529354	602558473	204	9.4	52.2	50	9	AU106755	AU106755	AU106755
C 132	9.6	53.3	34	17	AZ491280	AZ491280	1M0324E18	205	9.4	52.2	50	9	AU106758	AU106758	AU106758
C 133	9.6	53.3	37	9	A1240580	A1240580	qb52e10.r	206	9.4	52.2	50	9	AU106759	AU106759	AU106759
C 134	9.6	53.3	37	17	AZ476475	AZ476475	1M0295C24	207	9.4	52.2	50	9	AU106764	AU106764	AU106764
C 135	9.6	53.3	39	17	AZ666463	AZ666463	1M0548D08	208	9.4	52.2	50	9	AU107406	AU107406	AU107406
C 136	9.6	53.3	40	9	AA213154	AA213154	mm85c08.r	209	9.4	52.2	50	9	AU107665	AU107665	AU107665
C 137	9.6	53.3	40	17	AZ310280	AZ310280	1M0025K10	210	9.4	52.2	50	9	AU107667	AU107667	AU107667
C 138	9.6	53.3	41	17	B07643	B07643	CDCl1f Cr.1	211	9.4	52.2	50	9	AU107669	AU107669	AU107669
C 139	9.6	53.3	41	12	BG718339	BG718339	602696344	212	9.4	52.2	50	14	R98157	R98157	vg66e08.r.1
C 140	9.6	53.3	41	13	BT465330	BT465330	603206653	213	9.4	52.2	50	17	AZ481318	AZ481318	1M0303B05
C 141	9.6	53.3	42	14	T51284	T51284	yd20g07..s1	214	9.4	52.2	50	17	BH639080	BH639080	1M00802C0
C 142	9.6	53.3	42	17	AZ654954	AZ654954	1M0529B11	215	9.2	51.1	22	17	AZ324102	AZ324102	AZ324102
C 143	9.6	53.3	43	13	AA231049	AA231049	mm08h06.r.2	216	9.2	51.1	23	17	AZ806883	AZ806883	2M0069B15
C 144	9.6	53.3	43	13	BT333375	BT333375	602996772	217	9.2	51.1	23	17	TA610400	TA610400	TA610400
C 145	9.6	53.3	43	17	AZ447897	AZ447897	1M0245G17	218	9.2	51.1	24	17	AZ866934	AZ866934	AZ866934
C 146	9.6	53.3	43	17	TA84B02Q	TA84B02Q	brucei	219	9.2	51.1	24	17	AZ982483	AZ982483	2M0263K16
C 147	9.6	53.3	44	9	AA930614	AA930614	vy67a03.r	220	9.2	51.1	27	17	AZ466814	AZ466814	1M0282G02
C 148	9.6	53.3	45	17	AZ862434	AZ862434	2M0170E10	221	9.2	51.1	27	17	AZ598057	AZ598057	AA871664
C 149	9.6	53.3	45	17	BH848090	BH848090	SALK_0674	222	9.2	51.1	28	9	AT769631	AT769631	wj25a04.x
C 150	9.6	53.3	46	9	A1182146	A1182146	uc64a11.r	223	9.2	51.1	28	17	AZ492195	AZ492195	1M0326I08
C 151	9.6	53.3	47	10	BE534847	BE534847	601231985	224	9.2	51.1	29	17	AZ759919	AZ759919	1M0553H09
C 152	9.6	53.3	49	9	AA103183	AA103183	mo17a06.r	225	9.2	51.1	29	17			

226	9.2	51.1	30	17	Az498972	Az498972	1M0336D06	C 299	9.2	51.1	50	9	AU106746	AU106746	AU106746	AU106746
C 227	9.2	51.1	30	17	Az658025	Az658025	1M0534N04	C 300	9.2	51.1	50	9	AU106749	AU106749	AU106749	AU106749
C 228	9.2	51.1	31	17	Az402417	Az402417	1M0169008	C 301	9.2	51.1	50	9	AU107180	AU107180	AU107180	AU107180
C 229	9.2	51.1	31	17	Az407129	Az407129	1M0176K10	C 302	9.2	51.1	50	9	AU107596	AU107596	AU107596	AU107596
C 230	9.2	51.1	32	13	Bj033001	Bj033001	Bj033001	C 303	9.2	51.1	50	9	AU107670	AU107670	AU107670	AU107670
C 231	9.2	51.1	32	14	T49101	T49101	Yb08B11 .r1	C 304	9.2	51.1	50	9	AA250719	AA250719	AA250719	AA250719
C 232	9.2	51.1	32	17	Az39655	Az39655	1M0071A13	C 305	9.2	51.1	50	9	AA233215	AA233215	AA233215	AA233215
C 233	9.2	51.1	32	12	Az618503	Az618503	1M0450P13	C 306	9.2	51.1	50	9	AA2853501	AA2853501	AA2853501	AA2853501
C 234	9.2	51.1	33	13	Bj073398	Bj073398	602335701	C 307	9.2	51.1	50	9	Az244350	Az244350	Az244350	Az244350
C 235	9.2	51.1	33	13	Bj082142	Bj082142	Bj082142	C 308	9.2	51.1	50	9	R69803	R69803	R69803	R69803
C 236	9.2	51.1	33	17	Az436820	Az436820	1M0238106	C 309	9.2	51.1	50	9	TA296B020	TA296B020	TA296B020	TA296B020
C 237	9.2	51.1	33	17	Az4780229	Az4780229	2M0017G24	C 310	9.2	51.1	50	9	Az978415	Az978415	Az978415	Az978415
C 238	9.2	51.1	33	17	TA247408Q	TA247408Q	TA247408Q	C 311	9.2	51.1	50	9	Az978415	Az978415	Az978415	Az978415
C 239	9.2	51.1	33	17	TA263603P	TA263603P	TA263603P	C 312	9.2	51.1	50	9	Az978415	Az978415	Az978415	Az978415
C 240	9.2	51.1	34	9	A1188358	A1188358	qf08C03 .x	C 313	9.2	51.1	50	9	Az476559	Az476559	Az476559	Az476559
C 241	9.2	51.1	34	9	AA259780	AA259780	va87B10 .r	C 314	9.2	51.1	50	9	BH011395	BH011395	BH011395	BH011395
C 242	9.2	51.1	35	14	N73483	N73483	1M0513A16	C 315	9.2	51.1	50	9	Az433900	Az433900	Az433900	Az433900
C 243	9.2	51.1	35	17	Az647296	Az647296	1M0017021	C 316	9.2	51.1	50	9	AA665943	AA665943	AA665943	AA665943
C 244	9.2	51.1	36	10	Az780266	Az780266	AV950606	C 317	9.2	51.1	50	9	AA665943	AA665943	AA665943	AA665943
C 245	9.2	51.1	36	10	AV950606	AV950606	AV950606	C 318	9.2	51.1	50	9	AA665943	AA665943	AA665943	AA665943
C 246	9.2	51.1	36	14	C00778	C00778	HUMGS000239	C 319	9.2	51.1	50	9	AA665943	AA665943	AA665943	AA665943
C 247	9.2	51.1	37	9	A1917811	A1917811	wb53C07 .x	C 320	9.2	51.1	50	9	Az438137	Az438137	Az438137	Az438137
C 248	9.2	51.1	37	17	Az810046	Az810046	2M0074C23	C 321	9.2	51.1	50	9	Az676784	Az676784	Az676784	Az676784
C 249	9.2	51.1	37	17	TA325G09P	TA325G09P	TA325G09P	C 322	9.2	51.1	50	9	B1151368	B1151368	B1151368	B1151368
C 250	9.2	51.1	39	12	BF032106	BF032106	60155956	C 323	9.2	51.1	50	9	Bj066180	Bj066180	Bj066180	Bj066180
C 251	9.2	51.1	39	14	D26027	D26027	HUMGS02394	C 324	9.2	51.1	50	9	Az654189	Az654189	Az654189	Az654189
C 252	9.2	51.1	39	17	Az331571	Az331571	1M0059N06	C 325	9.2	51.1	50	9	Az779073	Az779073	Az779073	Az779073
C 253	9.2	51.1	39	17	Az242459	Az242459	1M0203D07	C 326	9.2	51.1	50	9	Az602844	Az602844	Az602844	Az602844
C 254	9.2	51.1	39	17	Az386277	Az386277	2M0268J20	C 327	9.2	51.1	50	9	AB016905	AB016905	AB016905	AB016905
C 255	9.2	51.1	40	10	AV834421	AV834421	AV834421	C 328	9.2	51.1	50	9	AA929647	AA929647	AA929647	AA929647
C 256	9.2	51.1	40	13	B1546135	B1546135	603188514	C 329	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 257	9.2	51.1	41	10	AV955327	AV955327	AV955327	C 330	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 258	9.2	51.1	41	9	AA907625	AA907625	om10e08 .s	C 331	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 259	9.2	51.1	43	17	Az645543	Az645543	1M0080M23	C 332	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 260	9.2	51.1	43	17	Az663563	Az663563	1M0542021	C 333	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 261	9.2	51.1	44	17	BH635056	BH635056	1008002C1	C 334	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 262	9.2	51.1	44	17	Az787976	Az787976	2M0043J15	C 335	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 263	9.2	51.1	45	10	AV833283	AV833283	AV833283	C 336	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 264	9.2	51.1	45	12	BE907096	BE907096	601500842	C 337	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 265	9.2	51.1	45	17	Az662097	Az662097	1M0541D03	C 338	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 266	9.2	51.1	46	9	A1203788	A1203788	qf77B04 .x	C 339	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 267	9.2	51.1	46	9	A1431214	A1431214	sa22a01 .Y	C 340	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 268	9.2	51.1	46	14	N77017	N77017	yz83B09 .r1	C 341	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 269	9.2	51.1	46	17	Az815494	Az815494	2M0083C18	C 342	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 270	9.2	51.1	46	17	Az815494	Az815494	2M0083C18	C 343	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 271	9.2	51.1	49	9	A1416542	A1416542	sa10e02 .Y	C 344	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 272	9.2	51.1	49	9	A1875730	A1875730	ue83905 .x	C 345	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 273	9.2	51.1	49	10	AV960885	AV960885	u124B01 .x	C 346	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 274	9.2	51.1	49	17	Az309933	Az309933	1M0017G23	C 347	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 275	9.2	51.1	50	9	AA114351	AA114351	MBAPCE40	C 348	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 276	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 349	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 277	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 350	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 278	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 351	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 279	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 352	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 280	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 353	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 281	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 354	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 282	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 355	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 283	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 356	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 284	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 357	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 285	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 358	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 286	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 359	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 287	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 360	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 288	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 361	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 289	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 362	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 290	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 363	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 291	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 364	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 292	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 365	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 293	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 366	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 294	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 367	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 295	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 368	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 296	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 369	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 297	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 370	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA936967
C 298	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 371	9.2	51.1	50	9	AA936967	AA936967	AA936967	AA

372	9	50.0	43	9	AA861070	AA861070 ak32e03.s	445	9	50.0	50	9	AU107354	AU107354
373	9	50.0	43	9	AA564874	AA564874 nj01b02.s	446	9	50.0	50	9	AU107356	AU107356
374	9	50.0	43	14	H79092	H79092 yv77c12..s1	447	9	50.0	50	9	AU107358	AU107358
375	9	50.0	43	14	R71759	R71759 y185g09..s1	448	9	50.0	50	9	AU107359	AU107359
376	9	50.0	43	17	A2771147	A2771147 IM0573b07	449	9	50.0	50	9	AU107366	AU107366
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387	9	50.0	46	9	A1590143	A1590143 tol2e12..x	460	9	50.0	50	9	AU107378	AU107378
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389	9	50.0	47	9	AU255355	AU255355 H.sapiens D	462	9	50.0	50	9	AU107410	AU107410
390	9	50.0	47	13	B1412781	B1412781 602988478	463	9	50.0	50	9	AU107411	AU107411
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392	9	50.0	47	17	TA67C120	TA67C120 T..bruce1	465	9	50.0	50	9	AU107423	AU107423
393	9	50.0	47	17	TA96H120	TA96H120 T..bruce1	466	9	50.0	50	9	AU107424	AU107424
394	9	50.0	48	17	A2601433	A2601433 IM0419N11	467	9	50.0	50	9	AU107425	AU107425
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410	9	50.0	50	9	AU102767	AU102767 AU102767	483	9	50.0	25	17	BH865645	BH865645
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413	9	50.0	50	9	AU103386	AU103386 AU103386	486	9	50.0	28	17	A2491585	A2491585
414	9	50.0	50	9	AU103585	AU103585 AU103585	487	9	50.0	29	17	A2488981	A2488981
415	9	50.0	50	9	AU103585	AU103585 AU103585	488	9	50.0	29	17	A2803250	A2803250
416	9	50.0	50	9	AU103683	AU103683 AU103683	489	9	50.0	29	17	A2868876	A2868876
417	9	50.0	50	9	AU103696	AU103696 AU103696	490	9	50.0	30	17	A2655716	A2655716
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420	9	50.0	50	9	AU104230	AU104230 AU104230	493	9	50.0	32	13	Bj052038	Bj052038
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422	9	50.0	50	9	AU104233	AU104233 AU104233	495	9	50.0	33	17	A2772019	A2772019
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425	9	50.0	50	9	AU104268	AU104268 AU104268	498	9	50.0	34	9	AU255522	AU255522
426	9	50.0	50	9	AU104270	AU104270 AU104270	499	9	50.0	34	14	R96723	R96723
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431	9	50.0	50	9	AU104963	AU104963 AU104963	504	9	50.0	35	17	A2604061	A2604061
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437	9	50.0	50	9	AU105890	AU105890 AU105890	510	9	50.0	37	17	BH810697	BH810697
438	9	50.0	50	9	AU106018	AU106018 AU106018	511	9	50.0	38	12	BG669164	BG669164
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442	9	50.0	50	9	AU106763	AU106763 AU106763	515	9	50.0	39	13	Bj068725	Bj068725
443	9	50.0	50	9	AU107100	AU107100 AU107100	516	9	50.0	39	14	R77120	R77120
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C 519	8.8	48.9	40	9	AA197105	AA197105 zq09h01.r	C 592	8.8	48.9	50	9	AU102886	AU102886 AU102886
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C 521	8.8	48.9	40	13	B1060137	B1060137 BU060137	C 594	8.8	48.9	50	9	AU103237	AU103237 AU103237
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C 525	8.8	48.9	42	9	A1191530	A1191530 qe49a09.x	C 598	8.8	48.9	50	9	AU103342	AU103342 AU103342
C 526	8.8	48.9	43	9	AA680265	AA680265 ac66d06.x	C 599	8.8	48.9	50	9	AU103854	AU103854 AU103854
C 527	8.8	48.9	43	9	AA160376	AA160376 zot7h05.r	C 600	8.8	48.9	50	9	AU103857	AU103857 AU103857
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C 529	8.8	48.9	43	9	AA495842	AA495842 zvo5a2e2.r	C 602	8.8	48.9	50	9	AU104073	AU104073 AU104073
C 530	8.8	48.9	43	17	AZ762861	AZ762861 1M0358EP4	C 603	8.8	48.9	50	9	AU104074	AU104074 AU104074
C 531	8.8	48.9	44	17	BE367536	BE367536 601649333	C 604	8.8	48.9	50	9	AU104356	AU104356 AU104356
C 532	8.8	48.9	44	17	BH643282	BH643282 100805560	C 605	8.8	48.9	50	9	AU104694	AU104694 AU104694
C 533	8.8	48.9	45	12	BE691166	BE691166 602247257	C 606	8.8	48.9	50	9	AU105803	AU105803 AU105803
C 534	8.8	48.9	45	14	H91384	H91384 yu87h05.r1	C 607	8.8	48.9	50	9	AU105903	AU105903 AU105903
C 535	8.8	48.9	45	14	T92229	T92229 ye17f11.r1	C 608	8.8	48.9	50	9	AU106287	AU106287 AU106287
C 536	8.8	48.9	45	17	AZ328791	AZ328791 1M0052B18	C 609	8.8	48.9	50	9	AU106332	AU106332 AU106332
C 537	8.8	48.9	45	17	AZ791686	AZ791686 2M0041N10	C 610	8.8	48.9	50	9	AU106512	AU106512 AU106512
C 538	8.8	48.9	45	17	AZ806099	AZ806099 2M0067M20	C 611	8.8	48.9	50	9	AU106912	AU106912 AU106912
C 539	8.8	48.9	45	17	AA828900	AA828900 odt5h11.s	C 612	8.8	48.9	50	9	AU107022	AU107022 AU107022
C 540	8.8	48.9	46	9	AA836932	AA836932 of36c11.s	C 613	8.8	48.9	50	9	AU107087	AU107087 AU107087
C 541	8.8	48.9	46	9	AA916643	AA916643 oBh1905.s	C 614	8.8	48.9	50	9	AU107092	AU107092 AU107092
C 542	8.8	48.9	46	9	A1323615	A1323615 mp3bh09.x	C 615	8.8	48.9	50	9	AU107257	AU107257 AU107257
C 543	8.8	48.9	46	13	B1549257	B1549257 603189880	C 616	8.8	48.9	50	9	AU107258	AU107258 AU107258
C 544	8.8	48.9	46	13	BM393789	BM393789 50072-2-1	C 617	8.8	48.9	50	9	AU107259	AU107259 AU107259
C 545	8.8	48.9	46	14	M44070	M44070 yy30f05.r1	C 618	8.8	48.9	50	9	AU107260	AU107260 AU107260
C 546	8.8	48.9	46	14	R72707	R72707 yj35a01.r1	C 619	8.8	48.9	50	9	AU107261	AU107261 AU107261
C 547	8.8	48.9	46	14	M03482	M03482 ma07a09.r1	C 620	8.8	48.9	50	9	AU107622	AU107622 AU107622
C 548	8.8	48.9	46	14	W94066	W94066 zd96e11.s1	C 621	8.8	48.9	50	9	AU107623	AU107623 AU107623
C 549	8.8	48.9	46	17	AZ324779	AZ324779 1M0046D22	C 622	8.8	48.9	50	9	AU107685	AU107685 AU107685
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C 551	8.8	48.9	47	9	AA642360	AA642360 ns29f08.s	C 624	8.8	48.9	50	9	AU107717	AU107717 AU107717
C 552	8.8	48.9	47	9	AA828450	AA828450 oc6d08.s	C 625	8.8	48.9	50	9	AU107718	AU107718 AU107718
C 553	8.8	48.9	47	10	BE619449	BE619449 601473280	C 626	8.8	48.9	50	9	AU107719	AU107719 AU107719
C 554	8.8	48.9	47	14	H83798	H83798 yq4b06.s1	C 627	8.8	48.9	50	9	AU107720	AU107720 AU107720
C 555	8.8	48.9	47	14	R63276	R63276 y107e04.r1	C 628	8.8	48.9	50	9	AU107721	AU107721 AU107721
C 556	8.8	48.9	47	17	AZ399403	AZ399403 1M0165C17	C 629	8.8	48.9	50	9	AU107722	AU107722 AU107722
C 557	8.8	48.9	47	17	AZ462142	AZ462142 1M0269K14	C 630	8.8	48.9	50	9	AU107723	AU107723 AU107723
C 558	8.8	48.9	47	17	AZ583296	AZ583296 1M0378G15	C 631	8.8	48.9	50	9	AU107724	AU107724 AU107724
C 559	8.8	48.9	47	17	AZ840029	AZ840029 2M0136F21	C 632	8.8	48.9	50	9	AU107725	AU107725 AU107725
C 560	8.8	48.9	48	17	BH618704	BH618704 SALK_0395	C 633	8.8	48.9	50	9	AU107726	AU107726 AU107726
C 561	8.8	48.9	48	17	AZ331129	AZ331129 1M0056M21	C 634	8.8	48.9	50	9	AU107927	AU107927 AU107927
C 562	8.8	48.9	48	17	AZ801305	AZ801305 2M0059N01	C 635	8.8	48.9	50	13	BT708333	BT708333 BT708333
C 563	8.8	48.9	48	17	BH890043	BH890043 3526.1_12	C 636	8.8	48.9	50	17	AZ325789	AZ325789 AU068112
C 564	8.8	48.9	49	9	A1020998	A1020998 ua98e05.r	C 637	8.8	48.9	50	17	AZ639610	AZ639610 AU037F02
C 565	8.8	48.9	49	9	AA238955	AA238955 nc14a06.r	C 638	8.8	48.9	50	17	BH854860	BH854860 AU0421104
C 566	8.8	48.9	49	12	BE592288	BE592288 602249170	C 639	8.8	48.9	50	17	TA119B07P	TA119B07P AU0464671
C 567	8.8	48.9	49	13	BI770218	BI770218 603053284	C 640	8.8	48.9	50	17	TA361B02P	TA361B02P AU076570
C 568	8.8	48.9	49	13	BI910486	BI910486 603067855	C 641	8.8	48.9	50	17	AA896852	AA896852 vyl1d08.r
C 569	8.8	48.9	49	14	W71090	W71090 me27h08.r1	C 642	8.8	48.9	50	17	AA954769	AA954769 on56d05.s
C 570	8.8	48.9	49	14	W80511	W80511 zh50h08.r1	C 643	8.8	48.9	50	14	CO1243	CO1243 HUGS00796
C 571	8.8	48.9	49	17	AZ397630	AZ397630 1M0162012	C 644	8.8	48.9	50	17	AZ308511	AZ308511 1M0011L06
C 572	8.8	48.9	49	17	AZ465494	AZ465494 1M0275O23	C 645	8.8	48.9	50	17	AZ424958	AZ424958 2M0197L05
C 573	8.8	48.9	49	17	AZ795452	AZ795452 2M0049M11	C 646	8.8	48.9	50	17	AZ9338825	AZ9338825 1M0460F07
C 574	8.8	48.9	49	17	AZ804582	AZ804582 2M0065O09	C 647	8.8	48.9	50	17	AZ622957	AZ622957 1M02667D11
C 575	8.8	48.9	49	17	AZ850753	AZ850753 2M0152B13	C 648	8.8	48.9	50	17	AZ661659	AZ661659 2M0064RP2
C 576	8.8	48.9	49	17	AZ850753	AZ850753 2M0152B13	C 649	8.8	48.9	50	17	AZ798424	AZ798424 2M0055C18
C 577	8.8	48.9	49	17	AZ850753	AZ850753 2M0152B13	C 650	8.8	48.9	50	17	BI412700	BI412700 602389191
C 578	8.8	48.9	49	17	AA933036	AA933036 co75e10.s	C 651	8.8	48.9	50	17	BI838550	BI838550 1M0040U12
C 579	8.8	48.9	49	17	AA933036	AA933036 co75e10.s	C 652	8.8	48.9	50	17	AZ3434231	AZ3434231 2M0030O16
C 580	8.8	48.9	49	17	AU102262	AU102262 AU102262	C 653	8.8	48.9	50	17	AZ792571	AZ792571 2M0045D12
C 581	8.8	48.9	49	17	AU102264	AU102264 AU102264	C 654	8.8	48.9	50	17	AZ818961	AZ818961 2M0089N13
C 582	8.8	48.9	49	17	AU102267	AU102267 AU102267	C 655	8.8	48.9	50	17	BF339740	BF339740 602034936
C 583	8.8	48.9	49	17	AU102268	AU102268 AU102268	C 656	8.8	48.9	50	17	BF339740	BF339740 602034936
C 584	8.8	48.9	49	17	AU102269	AU102269 AU102269	C 657	8.8	48.9	50	17	BF339740	BF339740 602034936
C 585	8.8	48.9	49	17	AU102270	AU102270 AU102270	C 658	8.8	48.9	50	17	BF339740	BF339740 602034936
C 586	8.8	48.9	49	17	AU102271	AU102271 AU102271	C 659	8.8	48.9	50	17	BF339740	BF339740 602034936
C 587	8.8	48.9	49	17	AU102272	AU102272 AU102272	C 660	8.8	48.9	50	17	BF339740	BF339740 602034936
C 588	8.8	48.9	49	17	AU102273	AU102273 AU102273	C 661	8.8	48.9	50	17	BF339740	BF339740 602034936
C 589	8.8	48.9	49	17	AU102274	AU102274 AU102274	C 662	8.8	48.9	50	17	BF339740	BF339740 602034936
C 590	8.8	48.9	49	17	AU102275	AU102275 AU102275	C 663	8.8	48.9	50	17	BF339740	BF339740 602034936

664	8.6	47.8	31	17	AZ481810	AZ481810	1M0306C21	737	8.6	47.8	46	17	AZ833980	AZ833980	2M0116K21
665	8.6	47.8	31	17	AZ620934	AZ620934	1M0453B23	738	8.6	47.8	47	9	AA087264	AA087264	mol2f10.r
666	8.6	47.8	31	17	AZ788442	AZ788442	2M0035G02	739	8.6	47.8	47	12	BG404659	BG404659	602420B1.r
667	8.6	47.8	32	13	B1223057	B1223057	602942007	740	8.6	47.8	47	17	AZ823060	AZ823060	2M0096B22
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669	8.6	47.8	32	13	B1032969	B1032969	B1032969	742	8.6	47.8	47	17	AL761639	AL761639	ArabiDops
670	8.6	47.8	32	17	AZ853979	AZ853979	2M0157H21	743	8.6	47.8	48	17	AL767745	AL767745	ArabiDops
671	8.6	47.8	33	17	AQ026498	AQ026498	EP(2)0755	744	8.6	47.8	49	9	AA758360	AA758360	zg45f01.s
672	8.6	47.8	33	17	AZ861903	AZ861903	2M0168A09	745	8.6	47.8	49	9	AA233183	AA233183	zrf6f08.s
673	8.6	47.8	34	17	AZ315997	AZ315997	1M0033023	746	8.6	47.8	49	10	AM100845	AM100845	sdf6b05.Y
674	8.6	47.8	35	9	AL658499	AL658499	AL658499	747	8.6	47.8	49	14	C20877	C20877	HUMS0000494
675	8.6	47.8	35	10	BE531379	BE531379	601231117	748	8.6	47.8	49	14	RS5033	RS5033	y176f02.s1
676	8.6	47.8	35	17	AZ775090	AZ775090	2M0007002	749	8.6	47.8	49	17	AZ817223	AZ817223	2M0086N19
677	8.6	47.8	36	12	BE735658	BE735658	601304404	750	8.6	47.8	49	17	AZ834261	AZ834261	2M0116G19
678	8.6	47.8	36	17	AQ026010	AQ026010	EP(2)0461	751	8.6	47.8	49	17	AZ850572	AZ850572	2M0152B03
679	8.6	47.8	37	9	AA149901	AA149901	z002f05.r	752	8.6	47.8	50	9	AM102365	AM102365	AM102365
680	8.6	47.8	37	10	AM250607	AM250607	2822076.5	753	8.6	47.8	50	9	AM102372	AM102372	AM102372
681	8.6	47.8	37	14	B0605582	B0605582	BR_1070	754	8.6	47.8	50	9	AM102373	AM102373	AM102373
682	8.6	47.8	37	17	AQ025921	AQ025921	1(2)K1010	755	8.6	47.8	50	9	AM102575	AM102575	AM102575
683	8.6	47.8	37	17	AZ384621	AZ384621	1M0142A13	756	8.6	47.8	50	9	AM102744	AM102744	AM102744
684	8.6	47.8	37	17	TA311D10Q	TA311D10Q		757	8.6	47.8	50	9	AM102745	AM102745	AM102745
685	8.6	47.8	38	10	BE285987	BE285987	601097946	758	8.6	47.8	50	9	AM103034	AM103034	AM103034
686	8.6	47.8	38	10	BE310314	BE310314	601087907	759	8.6	47.8	50	9	AM103034	AM103034	AM103034
687	8.6	47.8	38	17	AZ592430	AZ592430	1M0403B22	760	8.6	47.8	50	9	AM103606	AM103606	AM103606
688	8.6	47.8	38	17	AZ785597	AZ785597	2M0029C08	761	8.6	47.8	50	9	AM103608	AM103608	AM103608
689	8.6	47.8	39	9	AL784237	AL784237	AL784237	762	8.6	47.8	50	9	AM103612	AM103612	AM103612
690	8.6	47.8	39	9	AU254920	AU254920	AU254920	763	8.6	47.8	50	9	AM103612	AM103612	AM103612
691	8.6	47.8	39	12	BE788284	BE788284	602114017	764	8.6	47.8	50	9	AM103882	AM103882	AM103882
692	8.6	47.8	39	12	BG819250	BG819250	602781407	765	8.6	47.8	50	9	AM103886	AM103886	AM103886
693	8.6	47.8	39	14	H57425	H57425	y13811.s1	766	8.6	47.8	50	9	AM104152	AM104152	AM104152
694	8.6	47.8	39	17	AZ776938	AZ776938	2M0011F03	767	8.6	47.8	50	9	AM104160	AM104160	AM104160
695	8.6	47.8	39	17	CNS07GXQ	CNS07GXQ		768	8.6	47.8	50	9	AM104232	AM104232	AM104232
696	8.6	47.8	40	9	AA468566	AA468566	ne07e04.s	769	8.6	47.8	50	9	AM104403	AM104403	AM104403
697	8.6	47.8	40	13	B1544620	B1544620	603242263	770	8.6	47.8	50	9	AM104405	AM104405	AM104405
698	8.6	47.8	40	17	AZ796690	AZ796690	2M0052P23	771	8.6	47.8	50	9	AM104467	AM104467	AM104467
699	8.6	47.8	40	17	BH865895	BH865895	SALK.1000	772	8.6	47.8	50	9	AM104723	AM104723	AM104723
700	8.6	47.8	41	13	B1828498	B1828498	603078276	773	8.6	47.8	50	9	AM104726	AM104726	AM104726
701	8.6	47.8	41	17	AZ480375	AZ480375	1M0301A20	774	8.6	47.8	50	9	AM104733	AM104733	AM104733
702	8.6	47.8	41	17	AZ785555	AZ785555	2M0029G04	775	8.6	47.8	50	9	AM104738	AM104738	AM104738
703	8.6	47.8	42	9	AL585489	AL585489	AL585489	776	8.6	47.8	50	9	AM105421	AM105421	AM105421
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706	8.6	47.8	42	17	AZ309443	AZ309443	1M0013011	779	8.6	47.8	50	9	AM105500	AM105500	AM105500
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709	8.6	47.8	42	17	BH627368	BH627368	100707D00	782	8.6	47.8	50	9	AM105793	AM105793	AM105793
710	8.6	47.8	43	9	AA932697	AA932697	co074d06.s	783	8.6	47.8	50	9	AM105795	AM105795	AM105795
711	8.6	47.8	43	9	AT036497	AT036497	ue65g12.r	784	8.6	47.8	50	9	AM105800	AM105800	AM105800
712	8.6	47.8	43	9	AT098177	AT098177	ue31a07.x	785	8.6	47.8	50	9	AM105841	AM105841	AM105841
713	8.6	47.8	43	9	AT1437739	AT1437739	sa39a01.y	786	8.6	47.8	50	9	AM105846	AM105846	AM105846
714	8.6	47.8	43	9	AT186712	AT186712	uj56b03.x	787	8.6	47.8	50	9	AM105847	AM105847	AM105847
715	8.6	47.8	43	9	AT1971753	AT1971753	wr07g07.x	788	8.6	47.8	50	9	AM105901	AM105901	AM105901
716	8.6	47.8	43	9	AA625723	AA625723	ad10f02.s	789	8.6	47.8	50	9	AM106022	AM106022	AM106022
717	8.6	47.8	43	14	H56932	H56932	y07b01.s1	790	8.6	47.8	50	9	AM106288	AM106288	AM106288
718	8.6	47.8	43	17	AZ491975	AZ491975	1M0325P17	791	8.6	47.8	50	9	AM106292	AM106292	AM106292
719	8.6	47.8	43	17	AZ584834	AZ584834	1M0389E15	792	8.6	47.8	50	9	AM107600	AM107600	AM107600
720	8.6	47.8	44	17	AZ799781	AZ799781	2M0057K23	793	8.6	47.8	50	9	AM107631	AM107631	AM107631
721	8.6	47.8	44	17	AL449735	AL449735	AL449735	794	8.6	47.8	50	9	AM107632	AM107632	AM107632
722	8.6	47.8	44	17	AZ760710	AZ760710	1M0554F08	795	8.6	47.8	50	9	AM107929	AM107929	AM107929
723	8.6	47.8	44	17	AL760705	AL760705	ArabiDops	796	8.6	47.8	50	9	AM108013	AM108013	AM108013
724	8.6	47.8	45	10	AV950473	AV950473	AV950473	797	8.6	47.8	50	9	AM255145	AM255145	AM255145
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726	8.6	47.8	45	17	BH791506	BH791506	SALK_0600	799	8.6	47.8	50	14	D18207	D18207	MUSGS00477
727	8.6	47.8	46	9	AA703753	AA703753	ag78b06.r	800	8.6	47.8	50	17	U44315	U44315	ENU44315.As
728	8.6	47.8	46	9	AA722219	AA722219	zh21a09.s	801	8.6	47.8	50	17	TA215A01P	TA215A01P	
729	8.6	47.8	46	9	AT019594	AT019594	ua91a06.r	802	8.6	47.8	50	16	AT582256	AT582256	tg65f03.x
730	8.6	47.8	46	9	AT667606	AT667606	fd16e11.x	803	8.6	47.8	50	17	AZ481973	AZ481973	1M0306C12
731	8.6	47.8	46	9	AT1701058	AT1701058	wc78c06.x	804	8.6	47.8	50	17	AZ761740	AZ761740	1M0556A13
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733	8.6	47.8	46	9	AT1894320	AT1894320	mt69a11.x	806	8.6	47.8	50	17	AZ853501	AZ853501	2M0156A18
734	8.6	47.8	46	9	AA604908	AA604908	no85d08.s1	807	8.6	47.8	50	17	AT444134	AT444134	fb44a01.y
735	8.6	47.8	46	14	R72281	R72281	y189e08.s1	808	8.6	47.8	50	17	AZ437792	AZ437792	1M0226P04
736	8.6	47.8	46	17	AZ325750	AZ325750	1M0048H21	809	8.6	47.8	50	17	AZ795491	AZ795491	2M0049E15

C 810	8.4	46.7	23	17	AA6554495	AZ6554495	1M0530E20	883	8.4	46.7	38	12	BF11332
C 811	8.4	46.7	25	9	AA9174443	AA9174443	0M01E05.8	884	8.4	46.7	38	12	BF137365
C 812	8.4	46.7	25	9	AA993070	AA993070	0M01E06.7	C 885	8.4	46.7	38	17	AZ419855
C 813	8.4	46.7	25	9	AI539187	AI539187	TP8BH07.x	C 885	8.4	46.7	38	17	AZ447531
C 814	8.4	46.7	25	17	AZ335392	AZ335392	1M0055M18	887	8.4	46.7	38	17	AZ450095
C 815	8.4	46.7	27	17	AZ308445	AZ308445	1M0011J22	888	8.4	46.7	38	17	AZ816596
C 816	8.4	46.7	27	17	AZ966603	AZ966603	2M0237J12	889	8.4	46.7	39	14	CO23222
C 817	8.4	46.7	28	9	AA905471	AA905471	0M01E11.5	C 890	8.4	46.7	39	17	AZ286829
C 818	8.4	46.7	28	9	AI7905446	AI7905446	AI02E08.x	C 891	8.4	46.7	40	9	AA988668
C 819	8.4	46.7	28	17	AZ444108	AZ444108	1M0239J110	892	8.4	46.7	40	9	AI288030
C 820	8.4	46.7	28	17	AZ782046	AZ782046	2M0022M19	C 893	8.4	46.7	40	13	BI821604
C 821	8.4	46.7	29	17	AZ985140	AZ985140	2M0266H20	C 894	8.4	46.7	40	17	BH801678
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C 823	8.4	46.7	30	10	AA833957	AA833957	AV833957	C 896	8.4	46.7	40	17	TA168A07Q
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C 829	8.4	46.7	31	9	AI021071	AI021071	UB9F0C5.x	C 902	8.4	46.7	42	17	AI2770484
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C 833	8.4	46.7	31	9	AA243105	AA243105	ZX25C04.x	C 906	8.4	46.7	43	9	AI591196
C 834	8.4	46.7	31	10	AA9633388	AA9633388	AV9633388	C 907	8.4	46.7	43	9	AI591196
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C 1000 8.4 46.7 49 13 BF322803 mab33b03.

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ALIGNMENTS

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RESULT 1 43 bp mRNA linear EST 02-JUL-1999
LOCUS A1786712
DEFINITION u56bd03.x1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1923917 3 similar to SW:ALBU_RAT P02770 SERUM ALBUMIN
PRECUSOR: mRNA sequence.

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ACCESSION A1786712
VERSION A1786712
KEYWORDS GI:5334428
SOURCE mouse mouse.
ORGANISM Mus musculus.
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 43)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,E., Kohli,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The Mashu-HMT Mouse EST Project 1999
Unpublished (1999)

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TITLE JOURNAL
COMMENT Contact: Marra M/Mashu-NCI Mouse EST Project 1999
Washington University School of Medicine

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MGI:9680209
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
1..43
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1923917"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"

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FEATURES

```

BASE COUNT 10 a 9 c 14 g 10 t
ORIGIN
Query Match 74.4%; Score 13.4; DB 9; Length 43;
Best Local Similarity 93.3%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

RESULT 2 40 bp mRNA linear EST 06-NOV-1996
LOCUS A111398/c
DEFINITION mp10f06.r1 Life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA
clone IMAGE:568835 5' similar to TR:C881558 C881558 PHAS-I. [1] ;
RNA sequence.
ACCESSION A111398
VERSION A111398
KEYWORDS GI:1663279
SOURCE mouse mouse.
ORGANISM Mus musculus.
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The Mashu-HMT Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washu-HMT Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

```

```

TITLE JOURNAL
COMMENT Contact: Marra M/Mouse EST Project
Washington University School of Medicine

```

```

TITLE JOURNAL
COMMENT Contact: Marra M/Mouse EST Project
Washington University School of Medicine

```

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:343483

Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev1 from Amerham
High quality sequence stop: 9.

FEATURES

source

1. 40
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="568835"
/clone_lib="Life Tech mouse embryo 8 5dpc 10664019"
/issue_type="embryo"
/dev_stage="8.5dpc embryos"
/lab_host="DH10B"
/note="Organ: whole embryo; Vector: pCMV-SPORT2; Site: 1;
Salt: Site 2: Not; Cloned unidirectionally. Primer:
Oligo dt. 8.5dpc embryos. pCMV-SPORT2 vector."
BASE COUNT 6 a 16 c 15 g 3 t

ORIGIN

Query Match 73.3% Score 13.2; DB 9; Length 40;
Best Local Similarity 83.3% Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 CCCGGAGGCGAGTCTGGC 18
||||| 11 |||||
Db 38 CCCGCTGGAGACTCTGCG 21

RESULT 3

LOCUS B1246232 36 bp mRNA linear EST 17-JUL-2001
DEFINITION 60295877391 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5124378 5',
mRNA sequence.

ACCESSION B1246232.1 GI:14789788
VERSION
KEYWORDS

SOURCE

house mouse.
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L19M1304 Row: a Column: 19
High quality sequence stop: 36.

ORGANISM

house mouse.
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

FEATURES

1. 36
Location/Qualifiers
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="5124378"
/clone_lib="NCI_CGAP_L19"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site: 1; Not;
Site 2: Salt; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 7 a 17 g 4 t

ORIGIN

Query Match 67.8% Score 12.2; DB 13; Length 36;
Best Local Similarity 82.4% Pred. No. 6.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 CCCGGAGGCGAGTCTGG 17
||||| 11 |||||
Db 9 CCGGAGAGCGAGAACTCG 25

Query Match 67.8% Score 12.2; DB 13; Length 36;
Best Local Similarity 82.4% Pred. No. 6.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 CCCGGAGGCGAGTCTGG 17
||||| 11 |||||
Db 4 CCGGAGAGCGAGAACTCG 20

RESULT 4
LOCUS A1014269 50 bp mRNA linear EST 30-AUG-2001
DEFINITION A1014269 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ZRV61769, mRNA sequence.

ACCESSION A1014269
VERSION A1014269
KEYWORDS A1014269.1 GI:13553790
EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

1. 50
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="ZRV61769"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT 12 a 15 c 14 g 7 t 2 others

ORIGIN

Query Match 67.8% Score 12.2; DB 9; Length 50;
Best Local Similarity 82.4% Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 CCCGGAGGCGAGTCTGG 17
||||| 11 |||||
Db 9 CCGGAGAGCGAGAACTCG 25

RESULT 5

LOCUS A2824475 30 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0099001F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0099001 F, DNA sequence.

ACCESSION A2824475
VERSION A2824475.1 GI:12994383
KEYWORDS
SOURCE GSS.
ORGANISM house mouse.
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Relilly

TITLE
JOURNAL
COMMENT
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: 0 column: 01
Seq primer: CATTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1. .30
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0099001"
/clone_lib="Mouse 10Kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1, the vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
6 a 11 c 6 g 7 t

Query Match 65.6%; Score 11.8; DB 17; Length 30;
Best Local Similarity 86.7%; Pred. No. 1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCT 15
DB 11 CTTGGAGTCACTCT 25

RESULT 6
AA975650/c 42 bp mRNA linear EST 22-MAY-1998
LOCUS oq3d09.s1 NCI-CGAP_Kid6 Homo sapiens cDNA IMAGE:1591025 3'
DEFINITION similar to gp:M77172_cds1 ZINC FINGER PROTEIN 22 (HUMAN);, mRNA
sequence.
ACCESSION AA975650
VERSION AA975650.1 GI:3151442
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 42)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE
JOURNAL
COMMENT
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapb-remail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLMN at:
www.bio.linnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .42
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1591025"
/clone_lib="NCI-CGAP_Kid6"
/sex="mixed"
/tissue_type="kidney tumor"
/lab_host="SQR (kanamycin resistant)"
/note="Organ: kidney; Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5' GAATTCGGCAGAG 3' 3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3' Average insert size: 1.0 kb."

BASE COUNT
ORIGIN
10 a 16 c 7 g 9 t

Query Match 65.6%; Score 11.8; DB 9; Length 42;
Best Local Similarity 86.7%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGGAAGCAGTCTG 16
DB 29 CAGGAAGGAGTCTG 15

RESULT 7
A2815319 45 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0083A05R Mouse 10Kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG2M0083A05 R, DNA sequence.
ACCESSION A2815319
VERSION A2815319.1 GI:12985227
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 45)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0083 row: A column: 05
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends

FEATURES

High quality sequence stop: 45.
Location/Qualifiers

source

```
1. .45
/organism="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="U982M0083A05"
/clone.lib="mouse 10kb plasmid U982M library"
/sex="Male"
/lab.host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD22my. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (g11473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

BASE COUNT 5 a 14 c 12 g 14 t

Query Match 65.6%; Score 11.8; DB 17; Length 45;
Best Local Similarity 86.7%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAGGCGAGTGTGCG 18
||||| ||||| |||||
Db 30 GGAGTGCAGTTGCG 44

RESULT 8
B1252223/c 42 bp mRNA linear EST 17-JUL-2001
LOCUS 602953127F1 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5087239 5',
DEFINITION mRNA sequence.
ACCESSION B1252223
VERSION B1252223.1 GI:14802469
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 42)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov

Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov f column: 08
Plate: L10M1844 row: f column: 08
High quality sequence stop: 42.

FEATURES

source 1. .42
/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:5087239"

/clone.lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab.host="DH10B (phage-resistant)"
/note="Organ: Liver. Vector: pORF7. Site 1: XhoI; Site 2:
EcoRI. cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCCGCGAG(C). Size-selected by 500bp for average insert size
1.8kb. Library constructed by Ling Hong in the Laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH-MGC
Library."

BASE COUNT 4 a 20 c 13 g 5 t

Query Match 64.4%; Score 11.6; DB 13; Length 42;
Best Local Similarity 77.8%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGGAGCGAGTGTGCG 18
||||| ||||| |||||
Db 23 CCCGGCGGCGAGTGTGCG 6

RESULT 9
B1252484/c 42 bp mRNA linear EST 17-JUL-2001
LOCUS 602952948F1 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5087458 5',
DEFINITION mRNA sequence.
ACCESSION B1252484
VERSION B1252484.1 GI:14802986
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 42)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov

Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov f column: 11
Plate: L10M1844 row: o column: 11
High quality sequence stop: 42.

FEATURES

source

1. .42
/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:5087458"
/clone.lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab.host="DH10B (phage-resistant)"
/note="Organ: Liver. Vector: pORF7. Site 1: XhoI; Site 2:
EcoRI. cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCCGCGAG(C). Size-selected by 500bp for average insert size
1.8kb. Library constructed by Ling Hong in the Laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH-MGC
Library."

BASE COUNT 4 a 20 c 13 g 5 t

Query Match 64.4%; Score 11.6; DB 13; Length 42;
Best Local Similarity 77.8%; Pred. No. 1.3e+05;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGAGGAGCTGTGGC 18
||||| ||||| |||
Db 23 CCCGCGGCGCACTGGGC 6

RESULT 10
CNS07HVN/C
LOCUS
DEFINITION CNS07HVN 45 bp DNA linear GSS 03-OCT-2001
Anopheles gambiae GSS 77 end of clone 30P21 of library Notredame1
from strain PEST of Anopheles gambiae (African malaria mosquito),
genomic survey sequence.

ACCESSION AL611573
VERSION AL611573.1 GI:15962996
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
REFERENCE 1 (bases 1 to 45)
Genoscope.
AUTHORS Direct Submission
TITLE Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
2 (bases 1 to 45)
Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.
REFERENCE Direct Submission
AUTHORS Submitted (01-OCT-2001) BIKI, Institut Pasteur, 25, rue du Dr.
JOURNAL Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.

FEATURES
source
1. .45
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="30P21"
/clone_lib="Notredame1"
/note="end : 77"

BASE COUNT 9 a 6 c 12 g 18 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 17; Length 45;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGAGGAGCTGTGGC 18
||||| ||||| |||
Db 44 CCCATAGTCAGTCCGGC 27

RESULT 11
AUI02427/C
LOCUS
DEFINITION AUI02427 50 bp mRNA linear EST 30-AUG-2001
Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADKA02325, mRNA sequence.

ACCESSION AUI02427
VERSION AUI02427.1 GI:13551947
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale

TITLE
AUTHORS
JOURNAL
MEDLINE
COMMENT

JOURNAL mapping of mRNA start sites
MEDLINE EMBO Rep. 2 (5), 388-393 (2001)
21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADKA02325"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylflumarate treated U937 cells"

BASE COUNT 5 a 15 c 18 g 12 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 9; Length 50;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGAGGAGCTGTGGC 18
||||| ||||| |||
Db 28 CCAGGAGCGAGCTGTGC 11

RESULT 12
AUI02430/C
LOCUS
DEFINITION AUI02430 50 bp mRNA linear EST 30-AUG-2001
Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADS001588, mRNA sequence.

ACCESSION AUI02430
VERSION AUI02430.1 GI:13551950
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADS001588"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylflumarate treated U937 cells"

BASE COUNT 5 a 15 c 18 g 12 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 9; Length 50;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGCGC 18
 ||||| ||||| |||||
 Db 30 CCGAGAGCAGCAGCTGTC 13

RESULT 13
 AUI02431/C 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI02431 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION AUI02431 mRNA sequence.
 ACCESSION AUI02431
 VERSION AUI02431.1 GI:13551951
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
 ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
 ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 Diverse transcriptional initiation revealed by fine, large-scale
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 EMBO Rep. 2 (5), 388-393 (2001)
 21270072
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
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 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yutaka@ims.u-tokyo.ac.jp
 Suzuki,Y., Toshitomo Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
 ,S. Construction and characterization of a full length-enriched and
 a 5'-end enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
 Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="ADS01912"
 /clone_1lb="Sugano Homo sapiens cDNA library"
 /note="Differential display comparison of untreated and
 dimethylfumarate treated U937 cells"
 BASE COUNT 7 a 16 c 18 g 9 t
 ORIGIN

Query Match 64.4% Score 11.6; DB 9; Length 50;
 Best Local Similarity 77.8%; Pred. No. 1.4e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGCGC 18
 ||||| ||||| |||||
 Db 36 CCGAGAGCAGCAGCTGTC 19

RESULT 14
 A2821049 22 bp DNA linear GSS 20-FEB-2001
 LOCUS A2821049 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0093G07 R. DNA sequence.
 ACCESSION A2821049
 VERSION A2821049.1 GI:12990957
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT
 84112 USA
 Tel.: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0093 row: 6 column: 07
 Seq primer: CACACAGAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0093G07"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny: Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g1147321149b1AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 3 a 8 c 8 g 3 t
 ORIGIN

Query Match 63.2% Score 11.2; DB 17; Length 22;
 Best Local Similarity 81.2%; Pred. No. 1.9e+05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGTC 16
 ||||| ||||| |||||
 Db 17 CCGAGAGCAGCAGCTGCG 2

RESULT 15
 A2776661 25 bp DNA linear GSS 16-FEB-2001
 LOCUS A2776661 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0010C05 R. DNA sequence.
 ACCESSION A2776661
 VERSION A2776661.1 GI:12904460
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0010 row: C column: 05
Seq primer: CACACAGCAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1. 25
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C2M0010C05"
/clone_1lb="Mouse 10Kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb]|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 4 a 7 c 8 g 6 t
ORIGIN

Query Match 62.2%; Score 11.2; DB 17; Length 25;
Best Local Similarity 81.2%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCGAGGCGAGTCTG 16
II II IIIIIII II
Db 6 CCTGCAGCGACGTGTG 21

RESULT 16
AUI04235/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI04235 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP18127, mRNA sequence.
ACCESSION AUI04235
VERSION AUI04235.1 GI:13553756
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
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JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP18127"
/clone_1lb="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylflumate treated U937 cells"

BASE COUNT 6 a 13 c 18 g 13 t
ORIGIN

Query Match 62.2%; Score 11.2; DB 9; Length 50;
Best Local Similarity 81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CGGAGCGAGTCTGCGC 18
IIIIII IIIII I I
Db 37 CGGAGTCTAGTCGCTC 22

RESULT 17
AUI04249 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI04249 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP1819, mRNA sequence.
ACCESSION AUI04249
VERSION AUI04249.1 GI:13553770
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP1819"
/clone_1lb="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylflumate treated U937 cells"

BASE COUNT 12 a 16 c 13 g 9 t
ORIGIN

Query Match 62.2%; Score 11.2; DB 9; Length 50;
Best Local Similarity 81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCGAGGCGAGTCTG 16

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Db      9  CCCAGAGGCGCGCTG 24
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RESULT 18
LOCUS   AUI07261
DEFINITION AUI07261 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION ZR66C889, mRNA sequence.
VERSION   AUI07261.1 GI:13556782
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
           ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
           ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
           Diverse transcriptional initiation revealed by fine, large-scale
           mapping of mRNA start sites
JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE   21270072
COMMENT   Contact: Yutaka Suzuki
           Department of Virology
           Institute of Medical Science, University of Tokyo
           4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
           Email: yuzuki@ims.u-tokyo.ac.jp
           Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
           ,S. Construction and characterization of a full length-enriched and
           a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
Source    Location/Qualifiers
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           /clone="ZRV6C889"
           /clone_1lb="Sugano Homo sapiens cDNA library"
           /note="Differential display comparison of untreated and
           dimethylfumarate treated U937 cells"
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ORIGIN
Query Match 62.2%; Score 11.2; DB 9; Length 50;
Best Local Similarity 81.2%; Pred. No. 2, 1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCGAGGCGACTCTG 16
Db 33 CTCGGAGGCGACTCTG 48
RESULT 19
LOCUS   AZ974759/c
DEFINITION AZ974759 38 bp DNA linear GSS 27-APR-2001
           2M0249F02R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
           clone UUGC2M0249F02 R, DNA sequence.
ACCESSION AZ974759
VERSION   AZ974759.1 GI:13845986
KEYWORDS  GSS.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
           Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
           ,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
           and Wright,D., Weiss,R.
           Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss

```

```

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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0249 row: F column: 02
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.
FEATURES
Source    Location/Qualifiers
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           /organism="Mus musculus"
           /strain="C57BL/6J"
           /db_xref="taxon:10090"
           /clone="UUGC2M0249F02"
           /clone_1lb="Mouse 10kb plasmid UUGC2M library"
           /sex="Female"
           /lab_host="E. coli strain XL10-Gold, T1-resistant, F-."
           /note="Vector: PMD42nv: Purified genomic DNA from M.
           musculus C57BL/6J (female) was obtained from the Jackson
           Laboratory Mouse DNA Resource
           (http://www.jax.org/resources/documents/dnares/). The DNA
           was hydrodynamically sheared by repeated passage through a
           0.005 inch orifice at constant velocity. The sheared DNA
           was blunt end-repaired with T4 DNA polymerase and T4
           polynucleotide kinase. Adaptor oligonucleotides were
           ligated to the blunt ends in high molar excess. The
           adaptor DNA was purified and size-selected for a 9.5 to
           10.5 kb range using preparative agarose gel
           electrophoresis. Vector DNA was prepared from a derivative
           of pMD42 (g147321419b1AF129072.1), a copy-number
           inducible derivative of plasmid R1. The vector was ligated
           with adaptors complementary to the insert adaptors and
           purified. The sheared, adaptor mouse DNA was annealed to
           adaptor vector DNA, and transformed into
           chemically-competent E. coli XL10-Gold (Stratagene) cells
           and selected for ampicillin resistance."
BASE COUNT 7 a 9 c 14 g 8 t
ORIGIN
Query Match 60.0%; Score 10.8; DB 17; Length 38;
Best Local Similarity 85.7%; Pred. No. 3, 2e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCCGAGGCGACTC 14
Db 14 CCCGAGGCGACTC 1
RESULT 20
LOCUS   AZ991289/c
DEFINITION AZ991289 42 bp DNA linear GSS 27-APR-2001
           2M0275119F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
           clone UUGC2M0275119 F, DNA sequence.
ACCESSION AZ991289
VERSION   AZ991289.1 GI:13862528
KEYWORDS  GSS.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
           Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
           ,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
           and Wright,D., Weiss,R.
           Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss

```

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0275 row: 1 column: 19
 Seq primer: GGTGTGTAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 42.

FEATURES

source

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 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U08C2M0275I19"
 /clone_lib="Mouse 10kb plasmid U08C2M 1library"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv: Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN

9 a 15 c 12 g 6 t

Query Match 60.0%; Score 10.8; DB 17; Length 42;
 Best Local Similarity 85.7%; Pred. No. 3.2e+05;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGAGGCAGCTCTGG 17
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Db 37 GGAGGCAGCCTCG 24

RESULT 21

LOCUS

AL771267 43 bp DNA linear GSS 19-JUN-2002
 Arabidopsis thaliana T-DNA flanking sequence GK-178G11-013562,
 genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

GSS.
 thale cress.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
 and Weissshaar,B.
 A pipeline for automated high-throughput generation of FSTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines

TITLE

JOURNAL
 REFERENCE

2 Unpublished

AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weissshaar,B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics
 Unpublished
 3 (bases 1 to 43)
 Li,Y., Rosso,M., Strizhov,N. and Weissshaar,B.
 Direct Submission
 Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion close to or within gene At4g03970. The
 sequences are generated at the MPI for Plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 Plant Genomics program designated 'GABI'. Information on line
 availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES

source

1. .43
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-178G11-013562"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161. The lines contain one or more T-DNA
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

BASE COUNT
 ORIGIN

11 a 11 c 10 g 11 t

Query Match 60.0%; Score 10.8; DB 17; Length 43;
 Best Local Similarity 85.7%; Pred. No. 3.2e+05;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGAGCAGTCT 15
 ||||||| |||||

Db 2 CCGAGAGCAGTCT 15

RESULT 22

LOCUS

W05609/c 46 bp mRNA linear EST 23-APR-1996
 z885f01.r1 Soares_fetal_lung_NbH119w Homo sapiens cDNA clone
 IMAGE:299353 5' similar to SW:GSH2_RAT P46413 GLUTATHIONE
 SYNTHETASE ; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

W05609
 W05609
 W05609.1 GI:1278320
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 46)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1995)
 Contact: Wilson RK
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estevatson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality

FEATURES
source

Possible reversed clone: similarity on wrong strand
Seq primer: mob.REGA+ET
High quality sequence stop: 1.
Location/Qualifiers

1. .46
/organism="Homo sapiens"
/db_xref="GDB:1244277"
/db_xref="taxon:9606"
/clone="IMAGE:299353"
/clone.lib="Soares_fetal_lung_NbH19W"
/dev_stage="19 weeks"
/adb_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-GTGTACCACTGAGAGTGAGCGCGCAATTTTATTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbH19W."

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 60.0%; Score 10.8; DB 14: Length 46;
Matches 12: Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Matches 12: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGAGCGACTGCTG 16
|||||
Db 17 CCGAGACNCMGCTG 2

RESULT 23
AA863626 49 bp mRNA linear EST 11-MAR-1998
LOCUS vx06b04.f1 Soares_thymus_2NBMt Mus musculus cDNA clone
DEFINITION IMAGE:1263631.5' similar to SW:IRF7_MOUSE P70434 INTERFERON
REGULATORY FACTOR 7 ; mRNA sequence.
ACCESSION AA863626
VERSION AA863626.1 GI:2956105
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
1 (bases 1 to 49)
REFERENCE
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubaque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,D., Morris,M., Schellenberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:666183
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amerisham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source

1. .49
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1263631"
/clone.lib="Soares_thymus_2NBMt"
/sex="male"
/tissue_type="thymus"
/dev_stage="4 weeks"
/adb_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-GTGTACCACTGAGAGTGAGCGCGCAATTTTATTTT-3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 85.7%; Score 10.8; DB 9: Length 49;
Matches 12: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Matches 12: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GAAGCAGCTGCGC 18
|||||
Db 12 GAAGCAGCTGAC 25

RESULT 24
R82988/c 49 bp mRNA linear EST 04-AUG-1995
LOCUS yp10f11.f1 Soares breast 3mHbSt Homo sapiens cDNA clone
DEFINITION IMAGE:187053.5' similar to SP:A47285 A47285 MILK FAT GLOBULE
PROTEIN - HUMAN ; mRNA sequence.
ACCESSION R82988
VERSION R82988.1 GI:927832
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 49)
REFERENCE
AUTHORS Hillier,L., Clark,N., Dubaque,T., Elliston,K., Hawkins,M., Holman,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Roulifing,T., Soares,M., Tan,F., Tsvaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merk EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert size: 880
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL.
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source

1. .49
Location/Qualifiers

[illegible]

RESULT	26	
LOCUS	AZ610133/C	
DEFINITION	AZ610133	29 bp DNA linear GSS 13-DEC-2000
ACCESSION	U04435F16f Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0435F16 F, DNA sequence.	
VERSION	AZ610133	
KEYWORDS	AZ610133.1 GI:11732323	
SOURCE	GSS.	
ORGANISM	house mouse.	
REFERENCE	Mus musculus	
AUTHORS	Eumariyola, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)	
TITLE	Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0435 Row: F Column: 16 Seq primer: CGTGTAAACGACGCCAGCT Class: plasmid ends High quality sequence stop: 29. Location/Qualifiers 1..29	
FEATURES	/organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0435F16" /clone_lib="Mouse 10kb plasmid UUGC1M library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (qll4732114[gb AF129072.1]) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
BASE COUNT	4 a 15 c 4 g 6 t	
ORIGIN		
Query Match	58.9%; Score 10.6; DB 17; Length 29;	
Best Local Similarity	76.5%; Pred. No. 3.8e+05;	
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
CCCGAAGGCAGTCGG 17		
23 CCAGAAGGGGGTATGG 7		

RESULT 27
LOCUS T62015/C
DEFINITION yb97c06.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79114 5' similar to gb:J03600 ARACHIDONATE 5-LIPOXYGENASE (HUMAN); mRNA sequence.
ACCESSION T62015
VERSION T62015.1 GI:665258
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiswick, B., Chiswick, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estevenson.wustl.edu
Insert Size: 489
High quality sequence stops: 18 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Putative full length read
Insert Length: 489 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 18.
Location/Qualifiers
1. 31
/organism="Homo sapiens"
/db_xref="GDB:482731"
/db_xref="taxon:9606"
/clone="IMAGE:79114"
/clone_lib="Stratagene Lung (#937210)"
/sex="male"
/dev_stage="72 years"
/lab_host="SOI cells (kanamycin resistant)"
/note="Organ: Lung; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: OLI50
dr. normal lung. Average insert size: 1.0 kb; Uni-ZAP XR Vector: -3' adaptor sequence: 5' GAAATCGGACAG 3' -3' adaptor sequence: 5' CTCGAGCTTTTCTTTTCTTTT 3'."
BASE COUNT 6 a 11 c 10 g 4 t
ORIGIN

Query Match 58.9%; Score 10.6; DB 14; Length 31;
Best Local Similarity 76.5%; Pred. No. 3.8e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGCTGTG 17
||| ||||| |||||
Db 31 CCGGAGGCGAGGCTGTG 15

RESULT 28
LOCUS AZ953906/C
DEFINITION 2M0219B22F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0219B22 F, DNA sequence.
ACCESSION AZ953906
VERSION AZ953906.1 GI:13825133

KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 38)
AUTHORS Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duvall, B., Hamli, C., Islam, H., Longcore, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0219 row: B column: 22
Seq primer: CGTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 38.
Location/Qualifiers
1. 38
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0219B22"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD22nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (g1147211419b/AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptor and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 1 a 13 c 15 g 9 t
ORIGIN

Query Match 58.9%; Score 10.6; DB 17; Length 38;
Best Local Similarity 76.5%; Pred. No. 4e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCGGAGGCGAGCTGTG 18
||||| ||||| |||||
Db 21 CCGGAGGCGAGCGCGCC 5

RESULT 29
LOCUS AQ939867
DEFINITION hm19g513 C17B Mouse BAC library Mus musculus genomic, DNA sequence.
ACCESSION AQ939867
VERSION AQ939867.1 GI:9581521
KEYWORDS GSS.

SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 42)
TITLE	Clark, R.M., Marker, P.C. and Kingsley, D.M. A novel candidate gene for mouse and human preaxial polydactyly with altered expression in limbs of Hemimelic extra-toes mutant mice
JOURNAL	Genomics 67 (1), 19-27 (2000)
MEDLINE	20399563
COMMENT	Contact: Kingsley DM Dept. of Developmental Biology and Howard Hughes Medical Institute Stanford University Beckman Center B300-279 Campus Drive, Stanford, CA 94305, USA Fax: 650 725 7739 Email: kingsley@cgm.stanford.edu Mus musculus chromosome 5, Hammetoe (Hm) region, exon-trapped sequence 13 from D5Mit195 to D5Mit44 interval Class: exon-trapped.
FEATURES	Location/Qualifiers 1..42
SOURCE	/organism="Mus musculus" /strain="129" /db_xref="taxon:10090" /clone_lib="CITB Mouse BAC library" /sex="male" 14 c 10 g 10 t 1 others
BASE COUNT	7 a 14 c 10 g 10 t 1 others
ORIGIN	
Query Match	58.9%; Score 10.6; DB 17; Length 42;
Best Local Similarity	76.5%; Pred. No. 4e+05;
Matches 13: Conservative	0; Mismatches 4; Indels 0; Gaps 0.
QY	2 CCGGAAGCAGCTGTGGC 18 1 11111111111111111111
Db	16 CTGGAATGCTGACTGGC 32
RESULT 30	
A2770047/c	42 bp DNA linear GSS 16-FEB-2001
LOCUS	1M0571B19p Mouse 10kb plasmid U06C1M library Mus musculus genomic
DEFINITION	clone U06C1M0571B19 F, DNA sequence.
ACCESSION	A2770047
VERSION	A2770047.1
KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 42) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0571 row: B column: 19 Seq primer: CGTGTAAACGACGCGCAGT Class: plasmid ends High quality sequence stop: 42. Location/Qualifiers
FEATURES	

Source	1.. 42	58.9%	Score 10.6:	DB 17:	Length 42:
1.. 42	/organism="Mus musculus"				
	/strain="C57BL/6J"				
	/db_xref="taxon:10090"				
	/clone="U06C1M0571B19"				
	/clone_lib="Mouse 10kb plasmid U06C1M library"				
	/sex="Male"				
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"				
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[9b]A5129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."				
BASE COUNT	1 a 21 c 10 g 10 t				
ORIGIN					
Query Match	58.9%: Score 10.6: DB 17: Length 42:				
Best Local Similarity	76.5%: Pred. No. 4e+05; Indels 0; Gaps 0:				
Matches 13: Conservative	0; Mismatches 4; Indels 0; Gaps 0:				
QY	2 CCGGAGGCGAGTCTGGC 18				
	1 11 11111 1 111				
Db	21 CAGCGAGCGAGCGACGC 5				
RESULT 31					
H63217	43 bp mRNA linear EST 11-OCT-1995				
LOCUS	Y48f07.r1 Soares fetal liver spleen INTLS Homo sapiens cDNA clone IMAGE:208549.5, similar to SP:A46159 A46159 ISGF-3 91 KDA COMPONENT=INTERFERON-DEPENDENT POSITIVE-ACTING TRANSCRIPTION FACTOR (ISGF-3 84 KDA COMPONENT) - ; mRNA sequence.				
ACCESSION	H63217				
VERSION	H63217.1 GI:1018018				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 43)				
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Ellison,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maitra,M., Parsons,J., Rikhi,L., Rohlfing,T., Soares,M., Tan,F., Trevasxis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.				
TITLE	The Mashu-Merck EST Project				
JOURNAL	Unpublished (1995)				
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu Insert Size: 1223 High quality sequence starts: 1 High quality sequence stops: 1 Source: IMAGE Consortium, LBNL. This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.lbnl.gov) for further information. Trace considered overall poor quality				

Soares and M. Fatima Bonaldó. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBH19W."

BASE COUNT 10 a 13 c 10 g 16 t

Query Match 58.9%; Score 10.6; DB 9; Length 49;
Best Local Similarity 76.5%; Pred. No. 4.1e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCGGAAGCAGCTGCG 17
|| ||||| ||||| |||
Db 39 CCAGAGAGCAGCTGTG 23

RESULT 34
LOCUS AU108079/c 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU108079 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION ZR66C660, mRNA sequence.
VERSION AU108079
KEYWORDS AU108079.1 GI:13557601
SOURCE EST.
ORGANISM human.

REFERENCE
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isooga, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, T., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072

TITLE
JOURNAL
MEDLINE
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

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source

1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ZR66C660"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylflumarate treated O937 cells"
17 c 12 g 11 t 1 others

BASE COUNT 9 a 17 c 12 g 11 t 1 others

Query Match 58.9%; Score 10.6; DB 9; Length 50;
Best Local Similarity 76.5%; Pred. No. 4.1e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 CCGGAAGCAGCTGCG 18
|| ||||| ||||| |||
Db 33 CCTGAGCCAGTGAAGC 17

RESULT 35
LOCUS BG296675 50 bp mRNA linear EST 21-FEB-2001
DEFINITION BG296675 602393620P1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4505500 5', mRNA sequence.
ACCESSION BG296675
VERSION BG296675.1 GI:13059564
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 50)
NIH-MGC <http://mgc.nci.nih.gov/>.
Contact: Robert Strausberg, Ph.D.
Email: c9gabs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LRAM10379 row: 9 column: 05
High quality sequence stop: 50.

FEATURES
source

1. 50
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4505500"
/clone_lib="NIH_MGC_94"
/issue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site.1: NotI; Site.2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: This is a NIH-MGC Library."

BASE COUNT 10 a 14 c 16 g 10 t

Query Match 58.9%; Score 10.6; DB 12; Length 50;
Best Local Similarity 76.5%; Pred. No. 4.1e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 CCGGAAGCAGCTGCG 18
|| ||||| ||||| |||
Db 11 CCAGAGGCCCTGTGCG 27

RESULT 36
LOCUS AZ486623/c 22 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0314G14R Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0314G14 R, DNA sequence.
ACCESSION AZ486623
VERSION AZ486623.1 GI:10653578
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: adunne@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0314 row: G column: 14
Seq primer: CACACAGGAACAGCTATGAC

JOURNAL
COMMENT

Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22

FEATURES
source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U061M0314G14"
/clone_1lb="Mouse 10kb plasmid U061M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
5 t
a 8 c 3 g

BASE COUNT
ORIGIN

Query Match 57.8%; Score 10.4; DB 17; Length 22;
Best Local Similarity 91.7%; Pred. No. 4.5e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCCGAGAGCAG 12
1111111111
Db 15 CCCGAGAGCAG 4

RESULT 37
AZ595064 22 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0407L23f Mouse 10kb plasmid U061M library Mus musculus genomic
DEFINITION clone U061M0407L23 F, DNA sequence.
ACCESSION AZ595064
VERSION AZ595064.1 GI:11717254
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0407 row: L column: 23
Seq primer: CGTTGTAACGAGCGCCAGT

Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22

FEATURES
source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U061M0407L23"
/clone_1lb="Mouse 10kb plasmid U061M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
6 t
a 4 c 7 g

BASE COUNT
ORIGIN
Query Match 57.8%; Score 10.4; DB 17; Length 22;
Best Local Similarity 91.7%; Pred. No. 4.5e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GAAGCAGCTG 16
1111111111
Db 11 GAAGCAGCTG 22

RESULT 38
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LOCUS 1M0038L15f Mouse 10kb plasmid U061M library Mus musculus genomic
DEFINITION clone U061M0038L15 F, DNA sequence.
ACCESSION AZ318942
VERSION AZ318942.1 GI:10369225
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 33)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0038 row: L column: 15
Seq primer: CGTTGTAACGAGCGCCAGT

Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers
source

1. .43
/organism="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="UUC1M0430P22"
/clone_1lb="mouse 10kb plasmid UUC1M library"
/sex="Male"
/lab_hosts="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 14 a 9 c 8 g 12 t
ORIGIN
Query Match 57.8%; Score 10.4; DB 17; Length 43;
Best Local Similarity 91.7%; Pred. No. 5e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GAAGCAGTCTG 16
|||||
Db 27 GAAGCATTCTG 16

Search completed: December 2, 2002, 14:06:30
Job time : 1968 secs

